

FIGURE 1

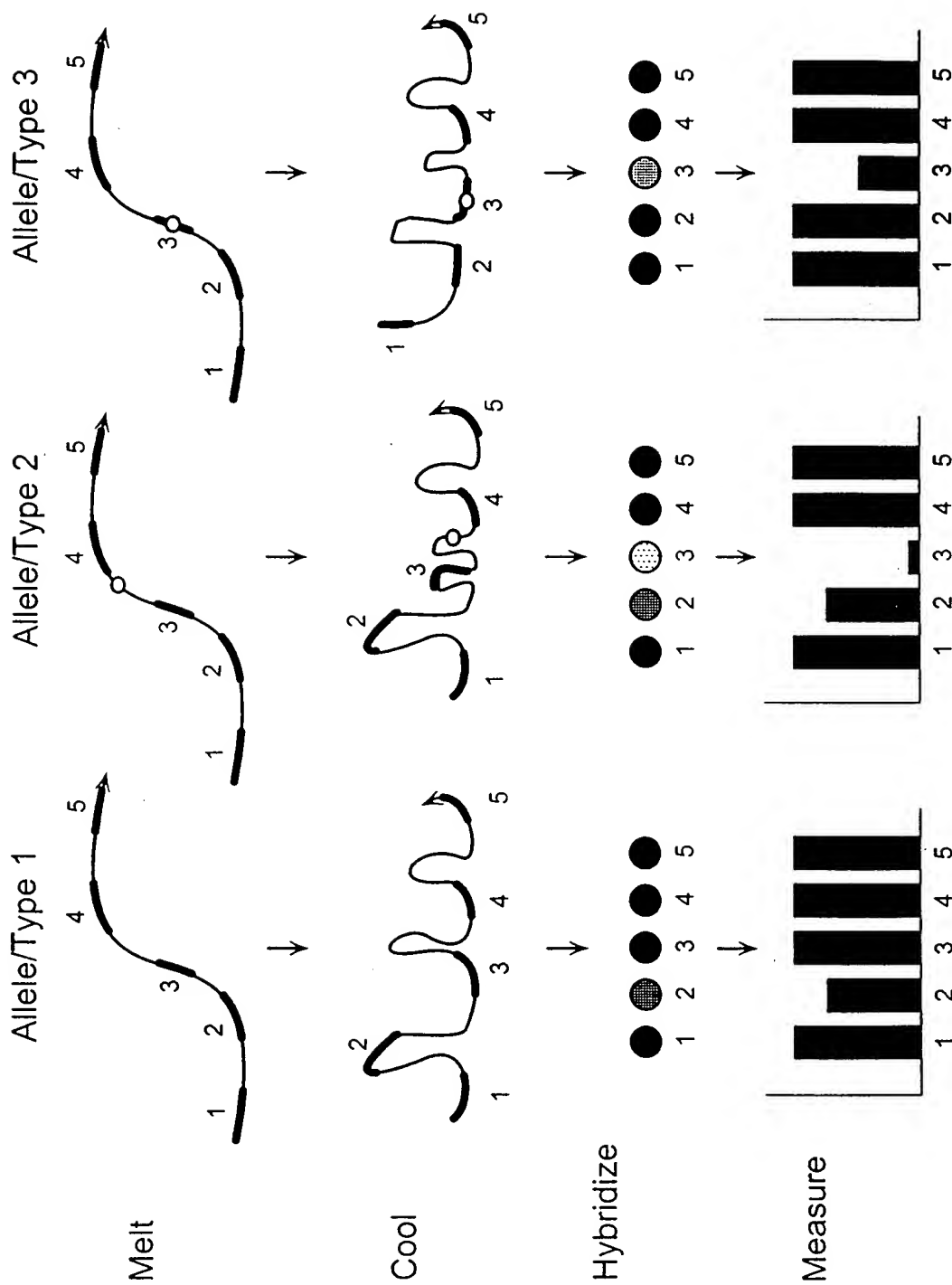


FIGURE 2

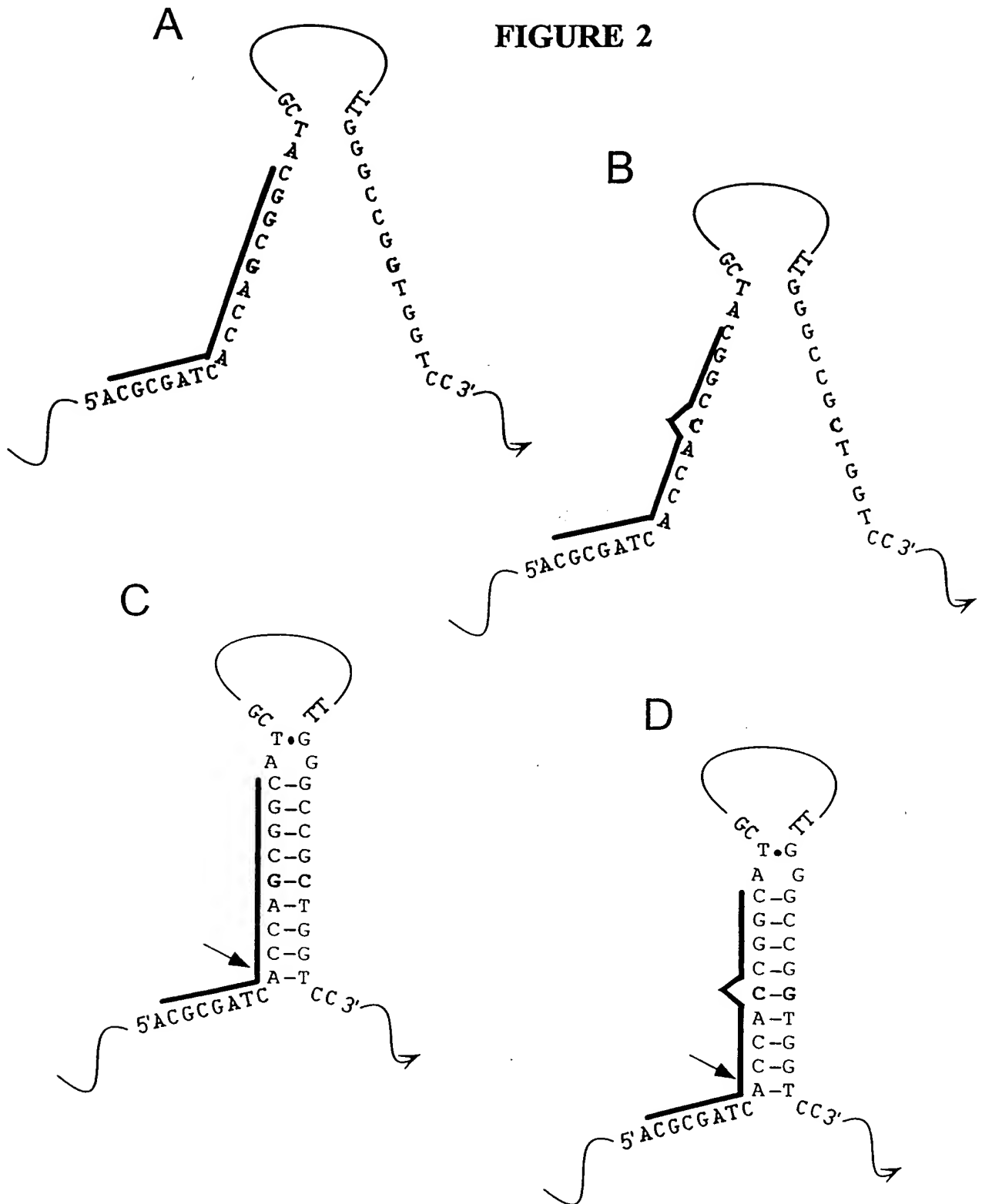


FIGURE 3

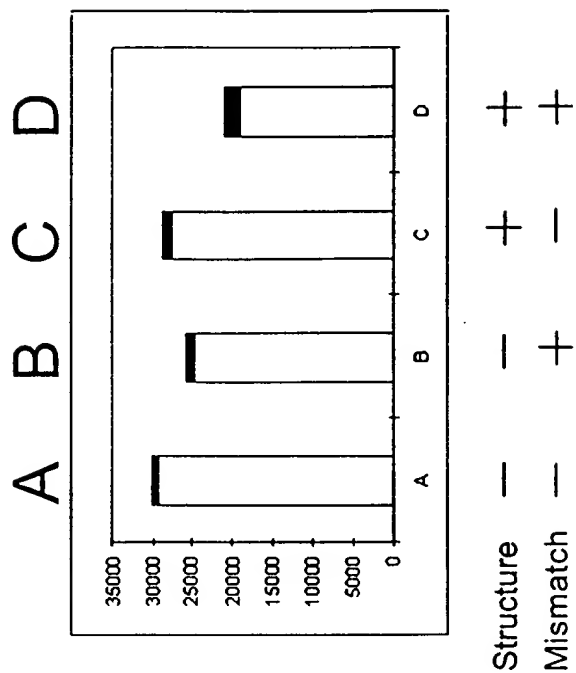
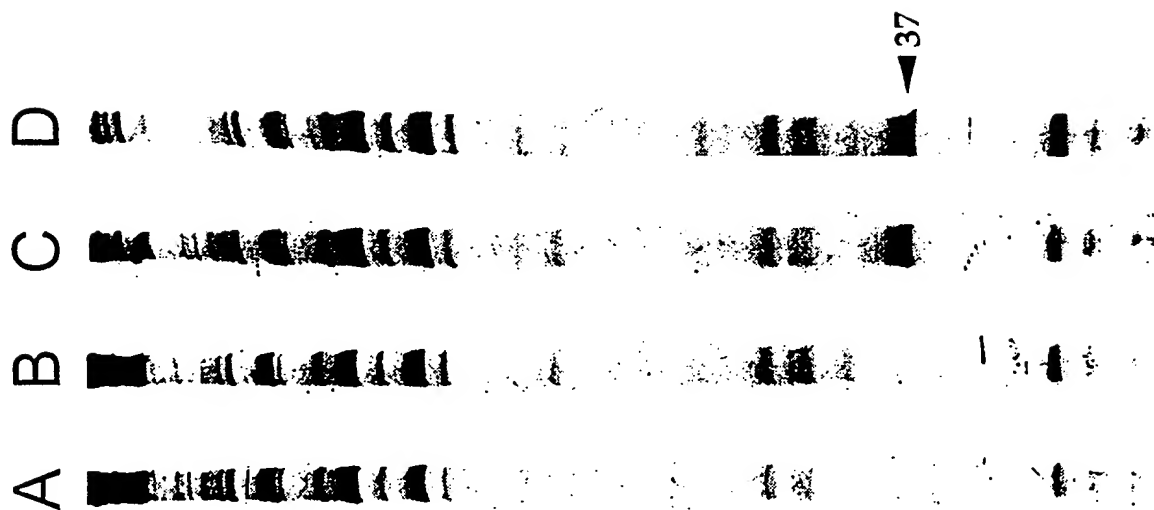


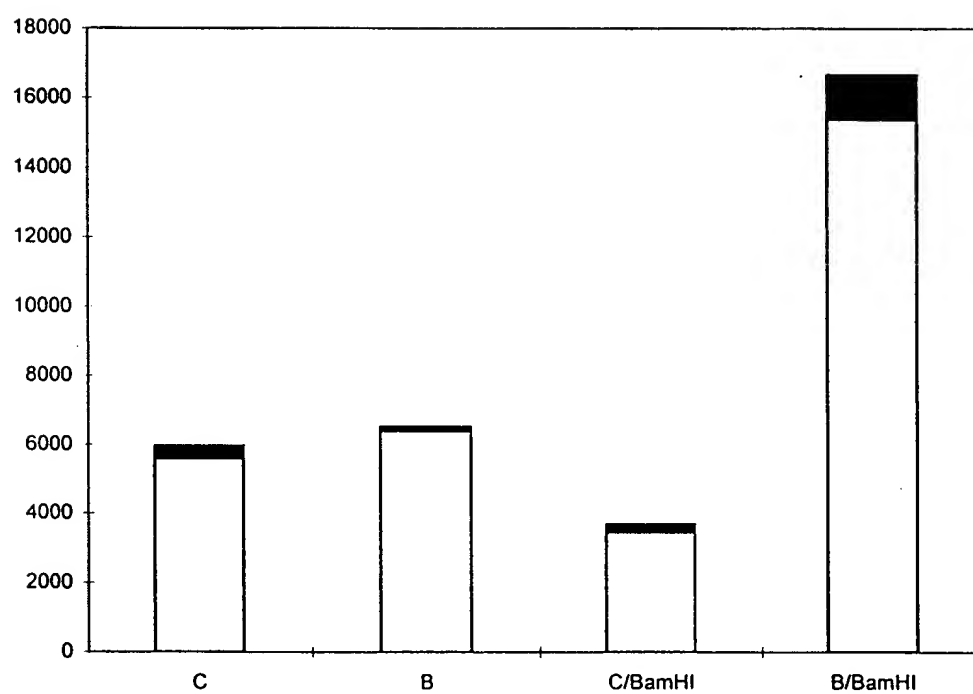
FIGURE 4

FIGURE 5

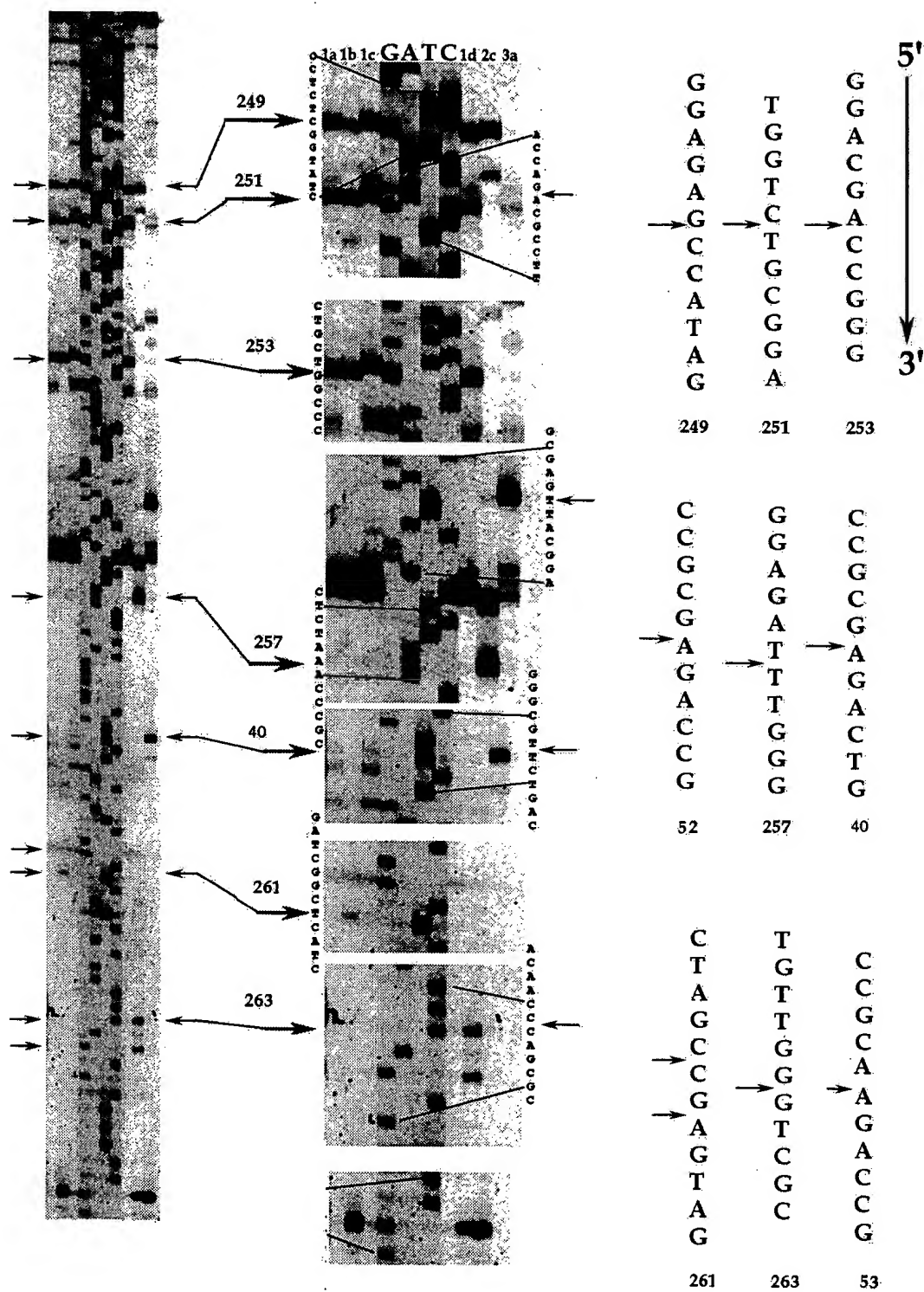


FIGURE 7

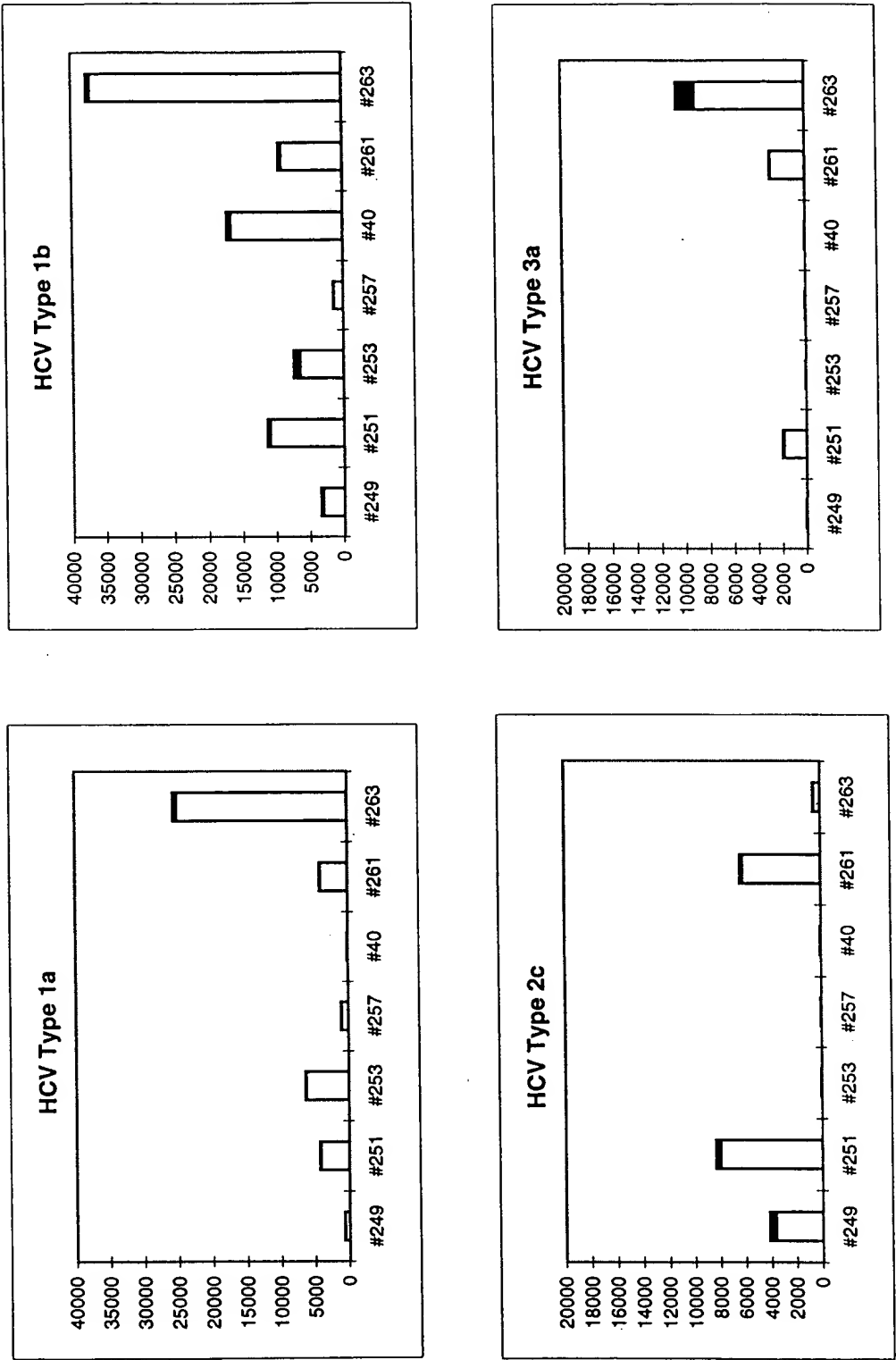


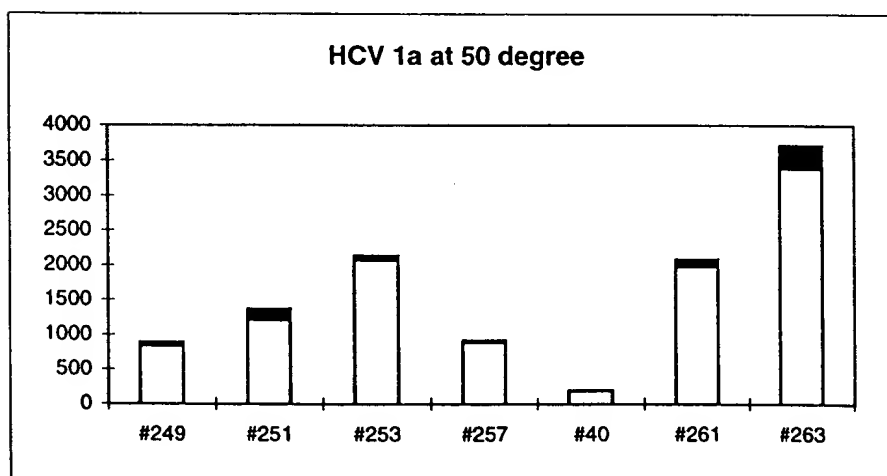
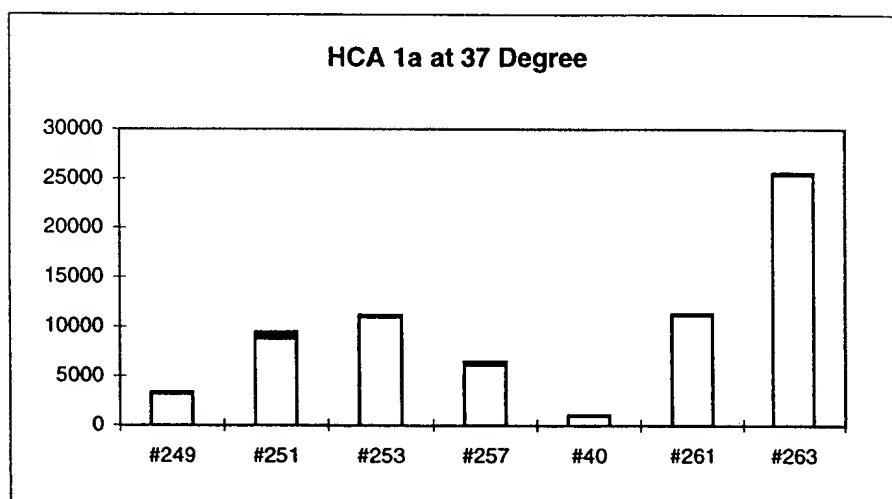
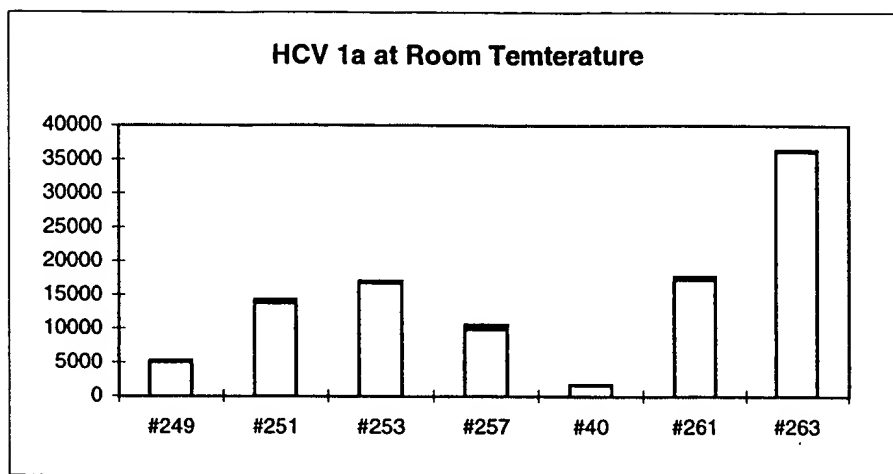
FIGURE 8A

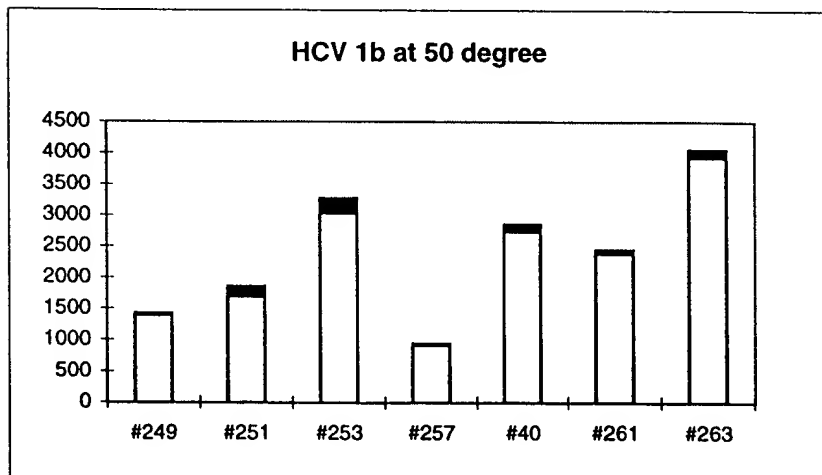
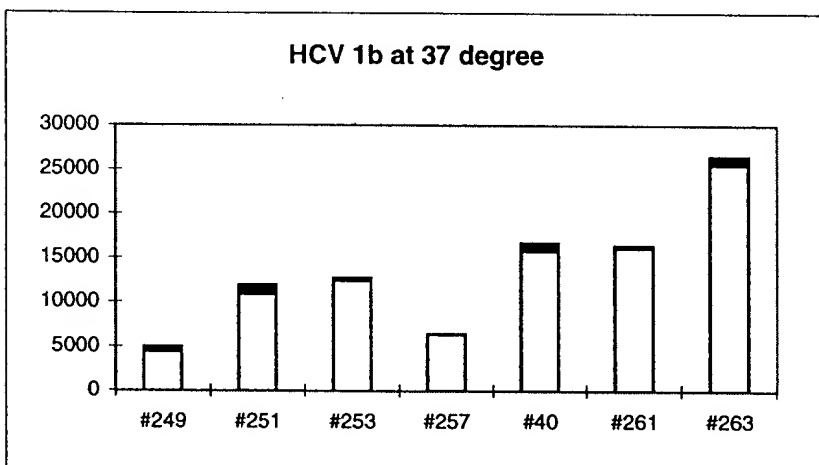
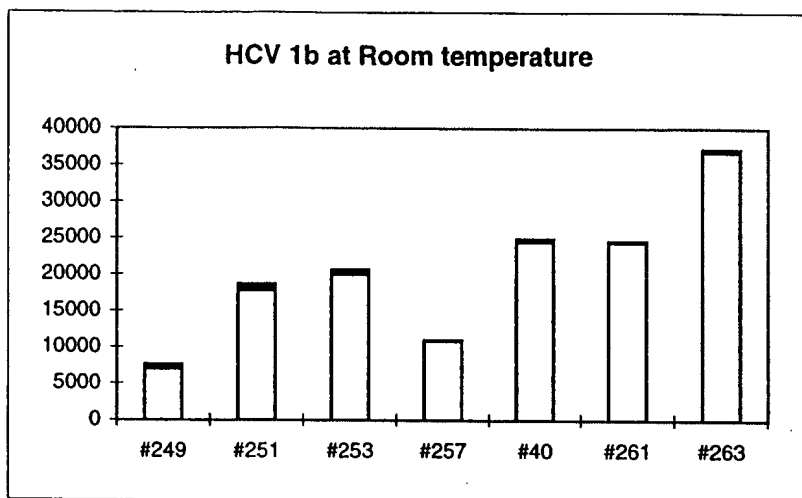
FIGURE 8B

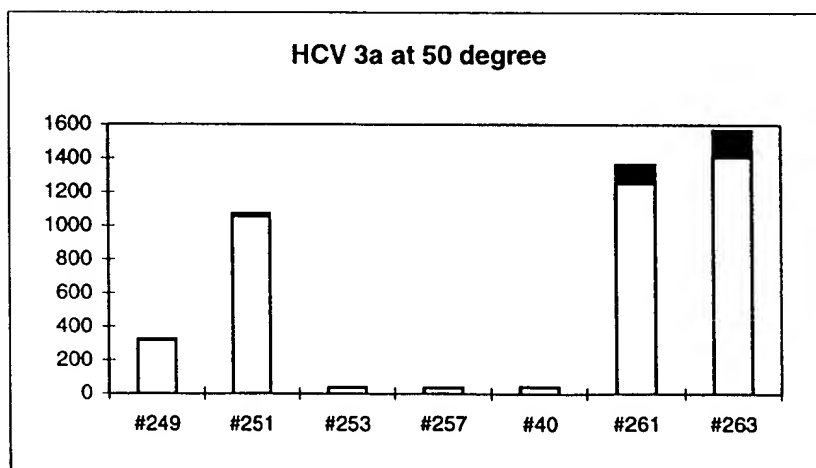
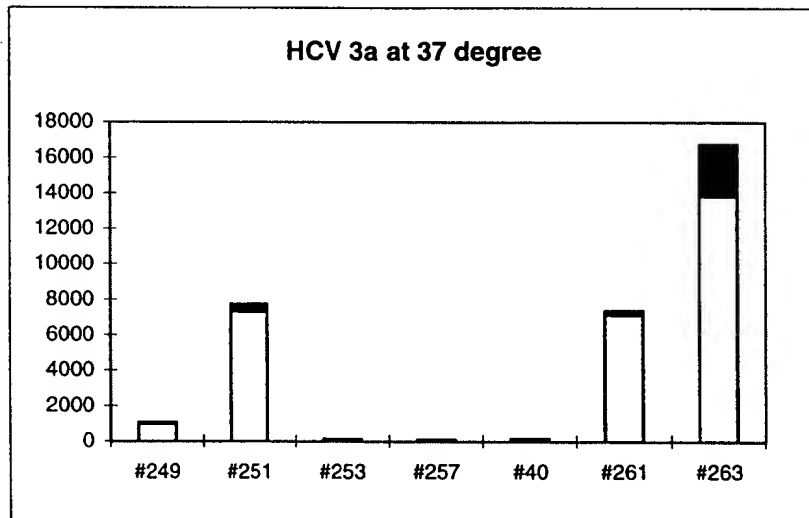
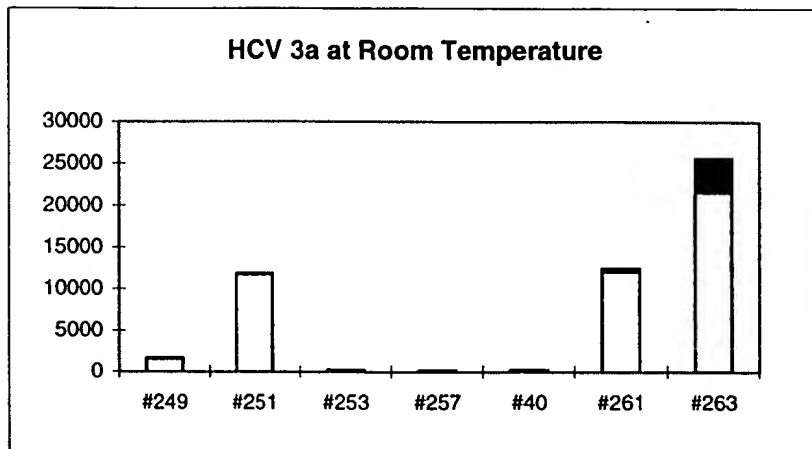
FIGURE 8C

FIGURE 9A

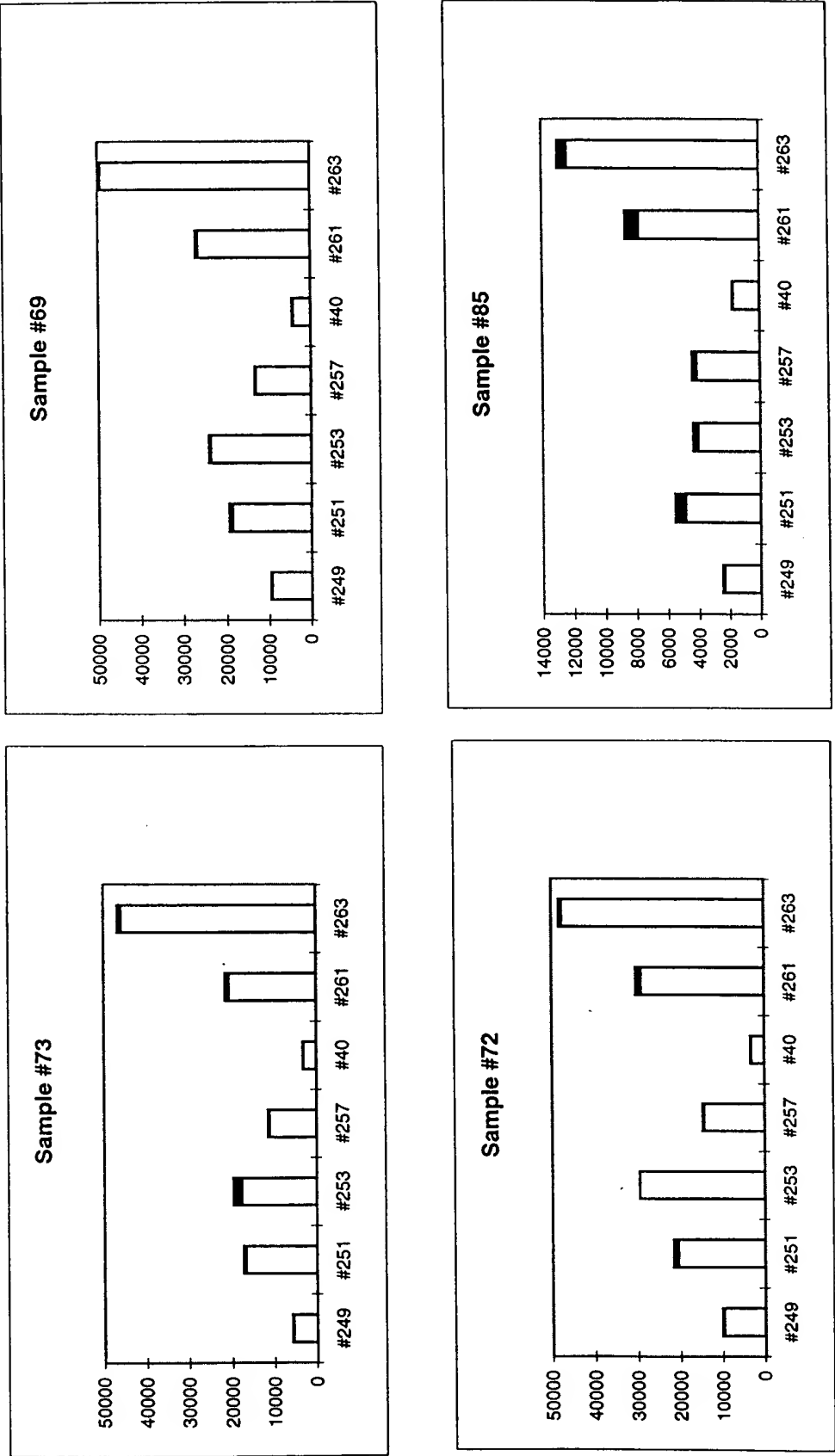


FIGURE 9B

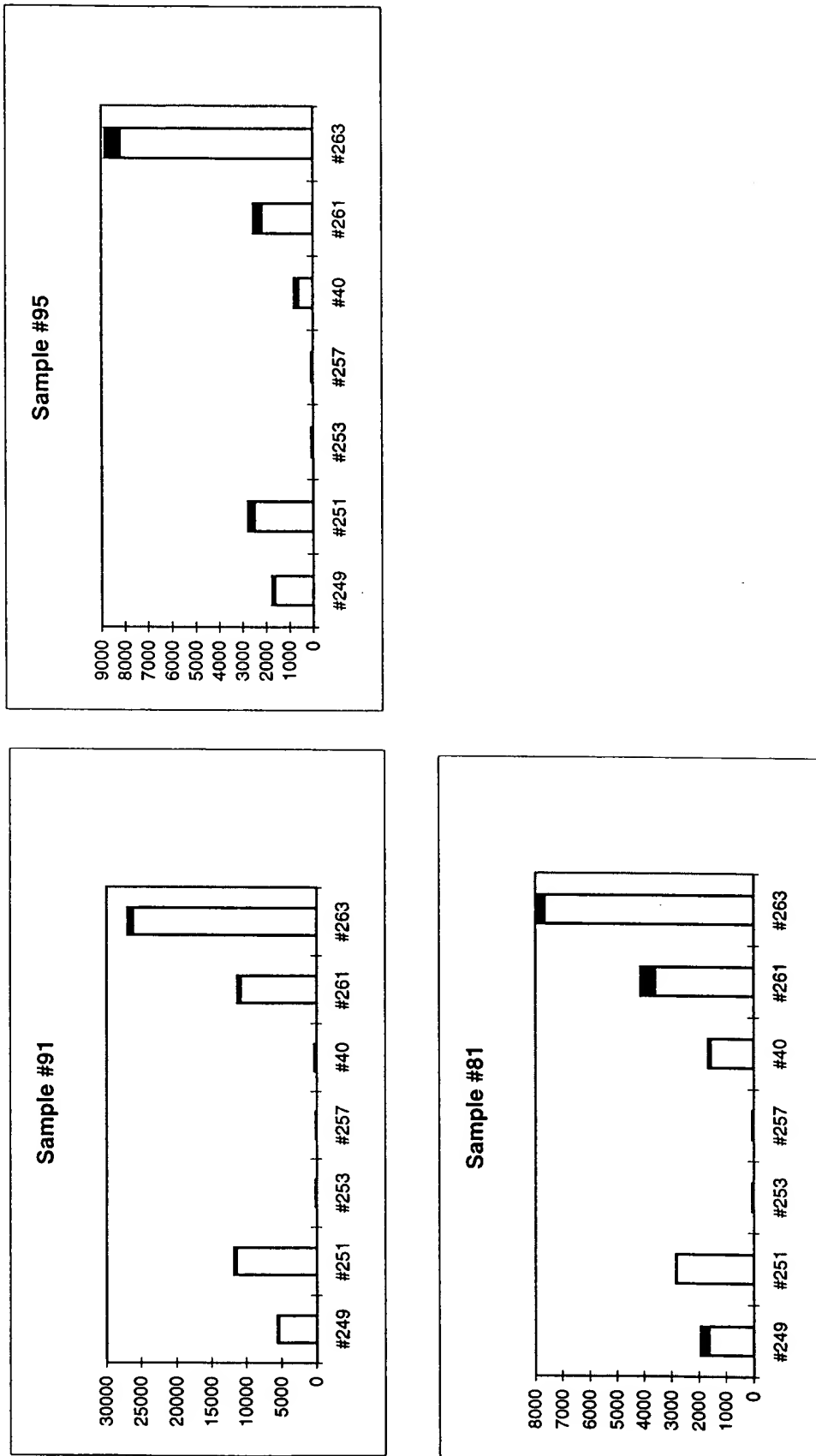


FIGURE 9C

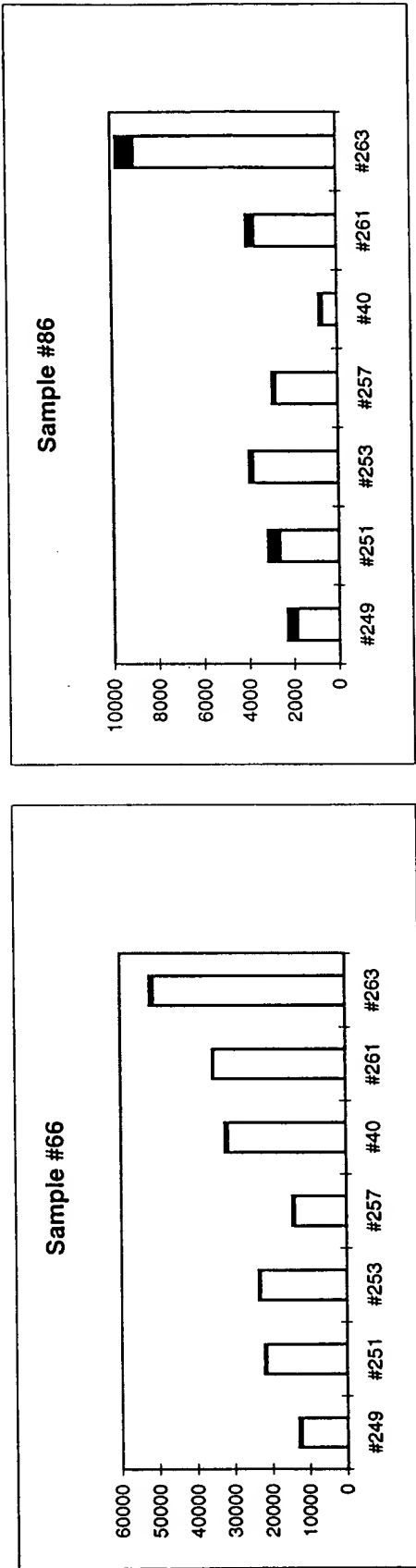


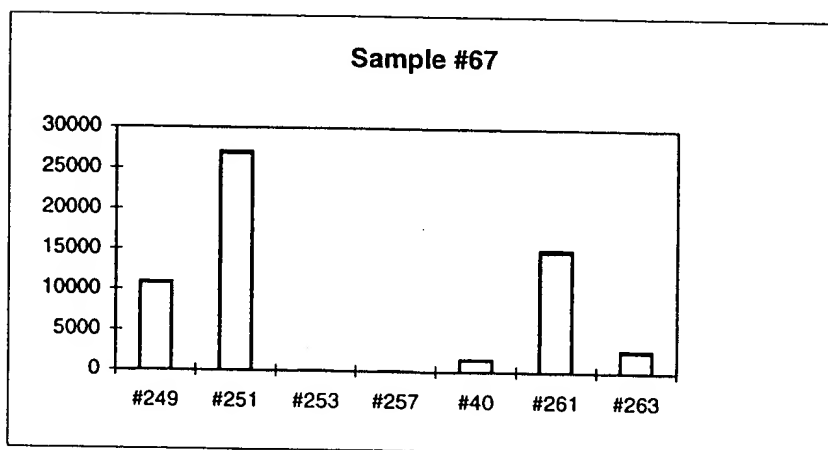
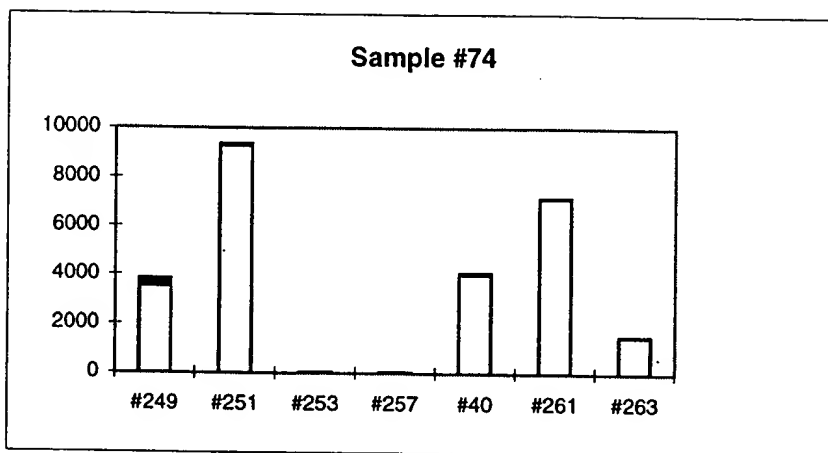
FIGURE 9D

FIGURE 10

#80

A
 G A
 T — A
 C — G
 T — A
 G — C
 T — A
 C — G
 G — C
 C — G

5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT -3'

#81

A
 G A
 T — A
 C — G
 T — A
 G — C
 T T
 C C
 G — C
 C — G

5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT -3'

#82

G^{AA}
 T T
 C T
 T T
 G T
 T T
 C T
 G T
 C T
 C T

5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT -3'

FIGURE 11A

#2) 5' Biotin

```

      |
      T   A
    C   G   A
    A   T—A
    G   C—G
    A   T—A
    C   G—C
    A   T—A
    G   C—G
    C   G—C
    G   C—G

```

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#FD91) 3' Biotin - CGAGAGACCA-5'

```

      A
    G   A
    T—A
    C—G
    T—A
    G—C
    T—A
    C—G
    G—C
    C—G

```

#80) 5' - FI-TGCTCTCTGGT TGGTCTCTCGTAAT-3'

#78) 3' - AGACCATTACCAGA -Biotin 5'

#4) 3' - GAGACCATTACCAGAG -Biotin 5'

#79) 3' - AGAGACCATTACCAGAGA -Biotin 5'



#116) 3' - AGAGACCAACCAGAGA -Biotin 5'

#117) 3' - TACCAGAGA -Biotin 5'

#118) 3' - AGAGACCAT -5'

FIGURE 11B

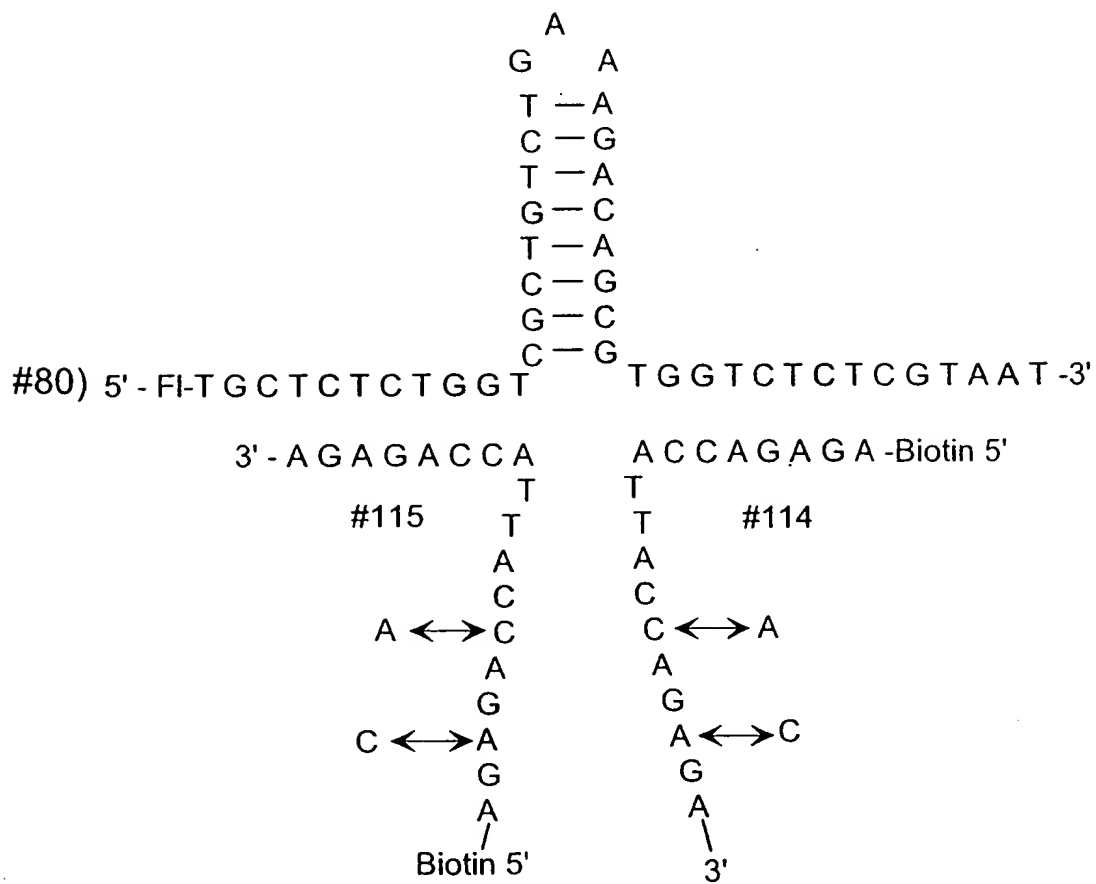
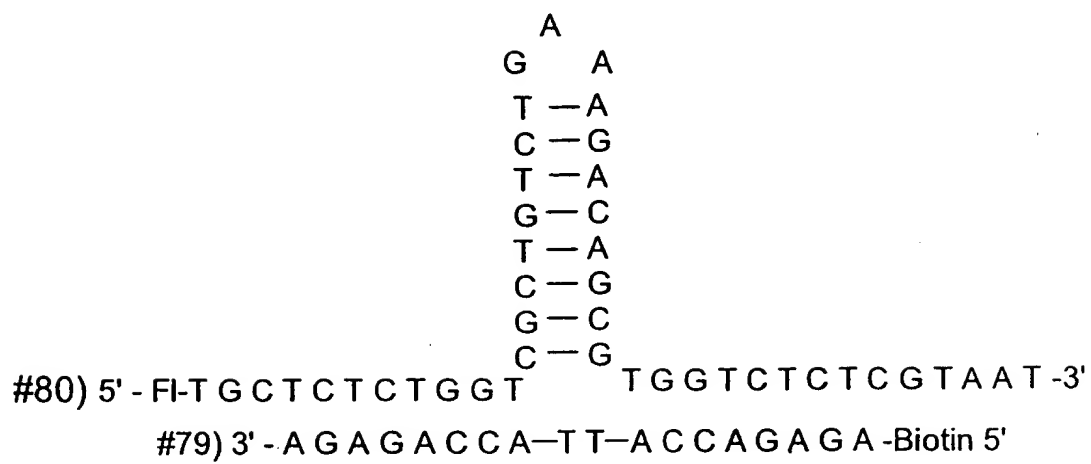
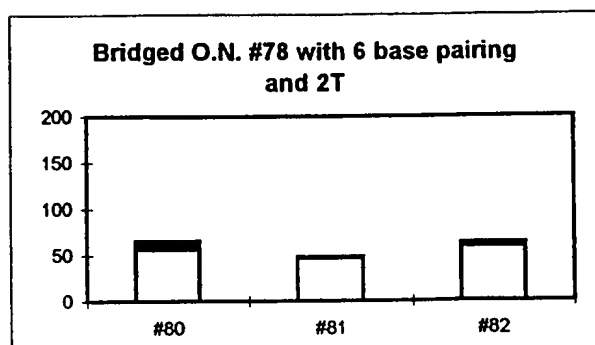
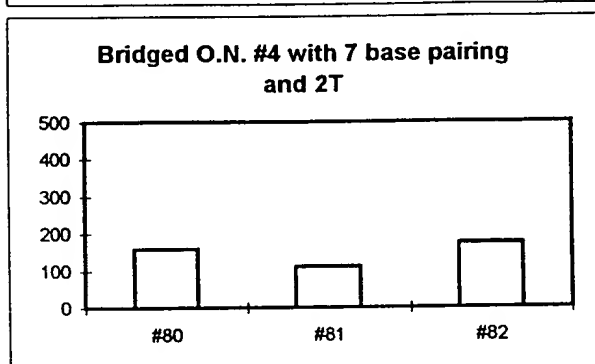


FIGURE 12

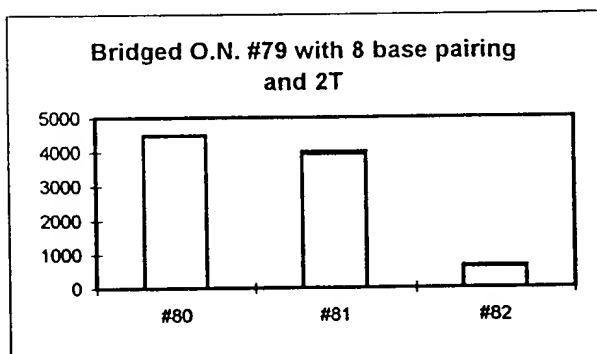
A



B



C



D

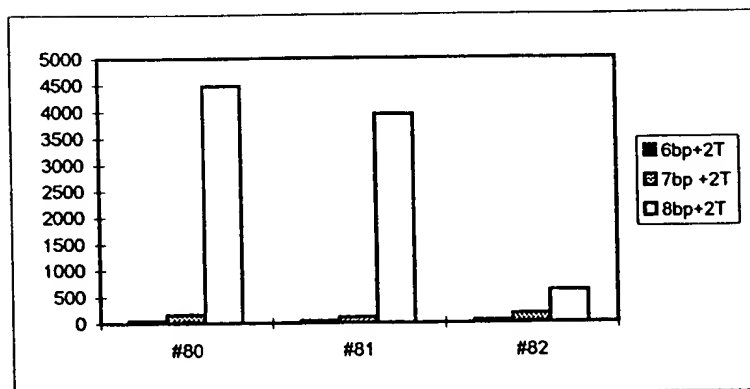


FIGURE 13A

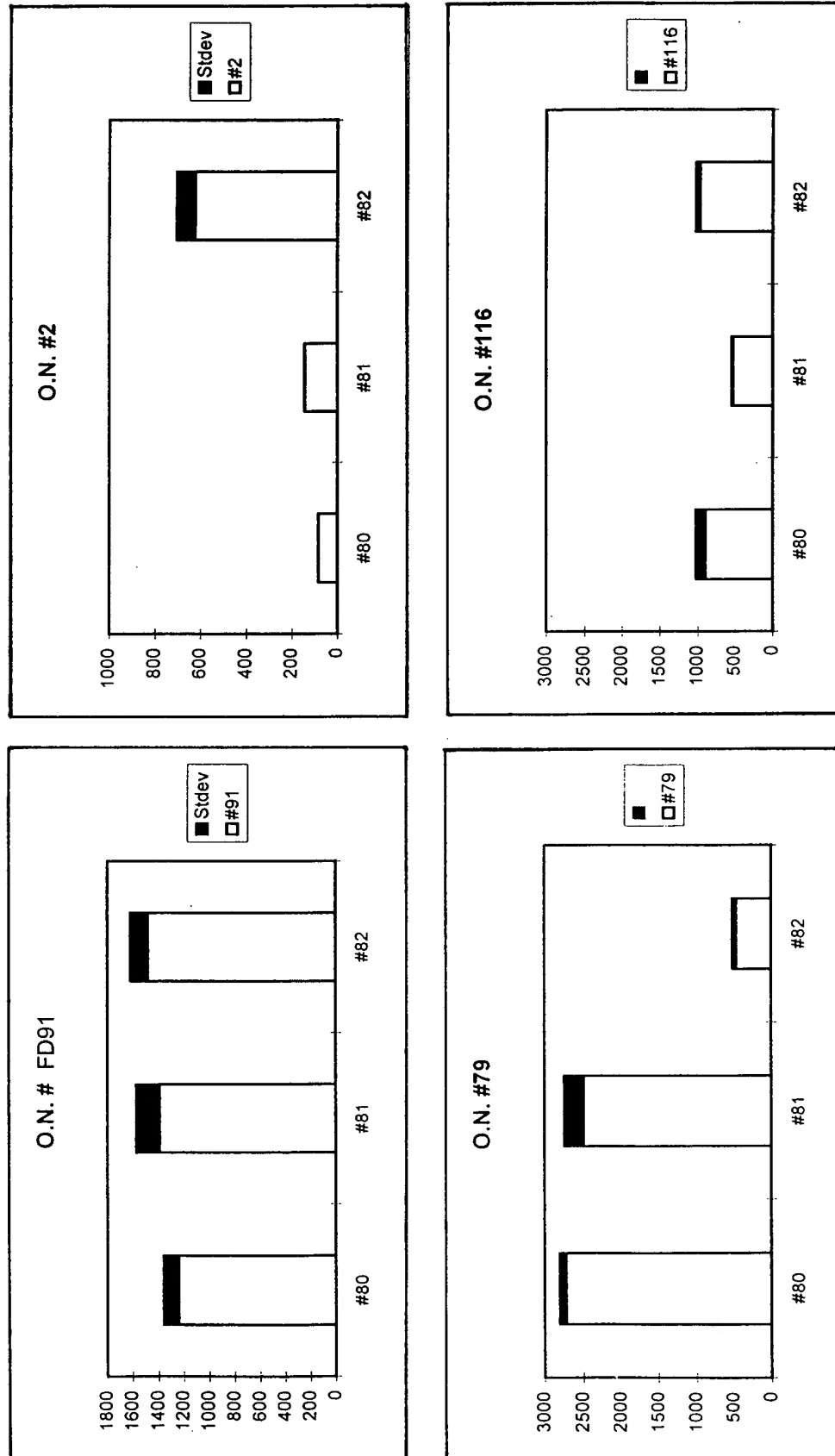


FIGURE 13B

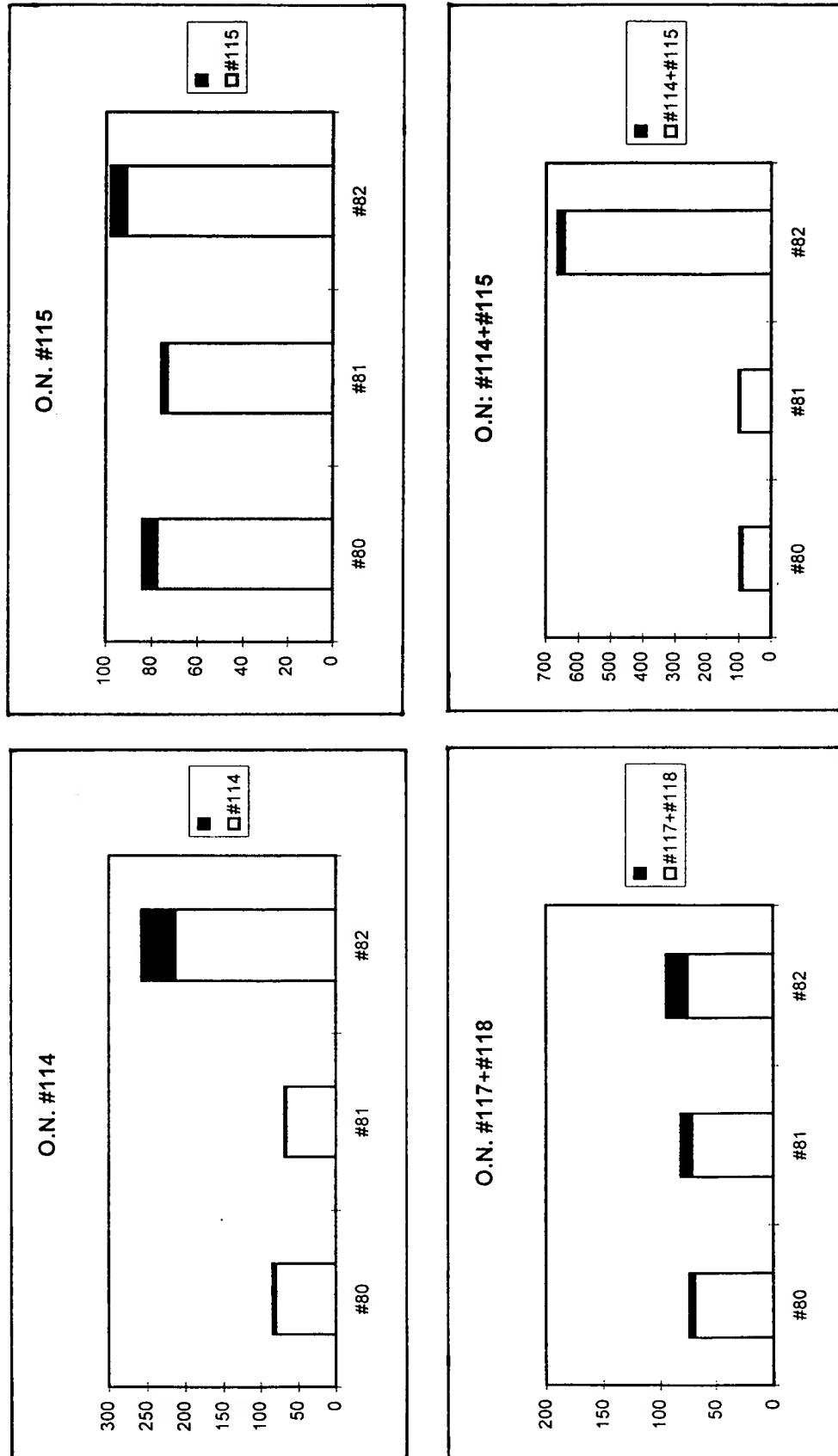


FIGURE 14

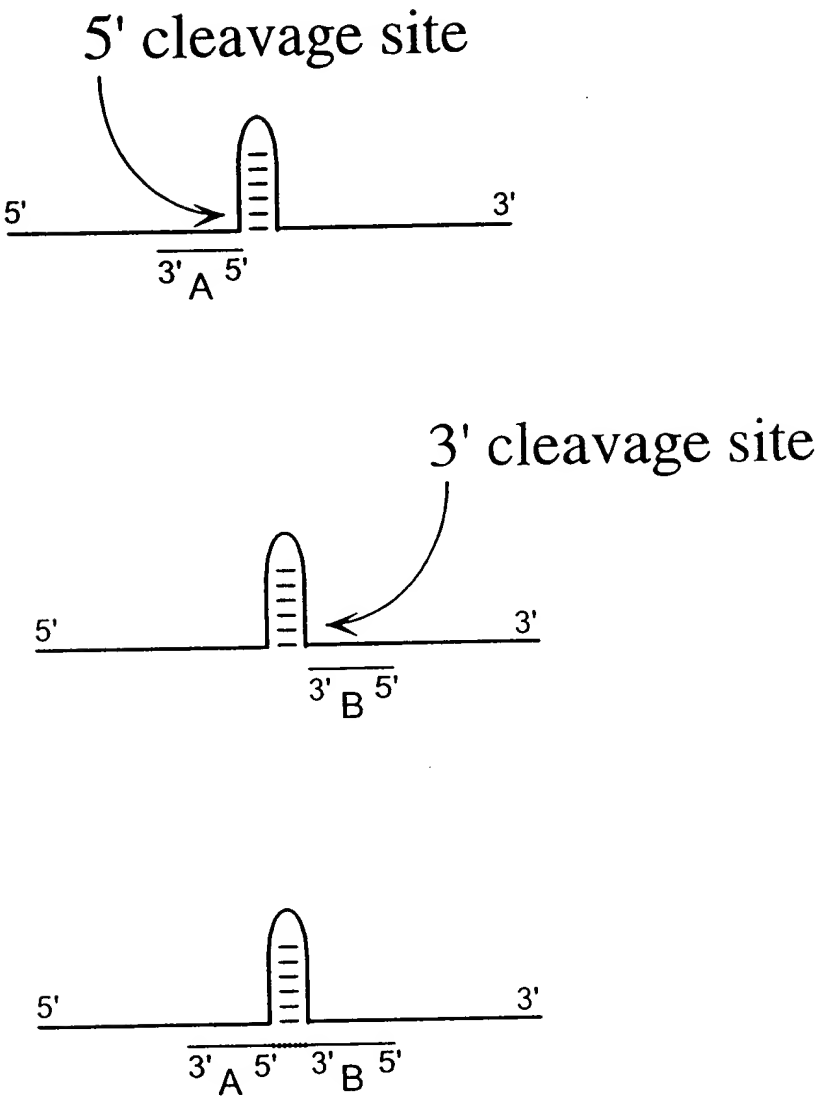


FIGURE 16A

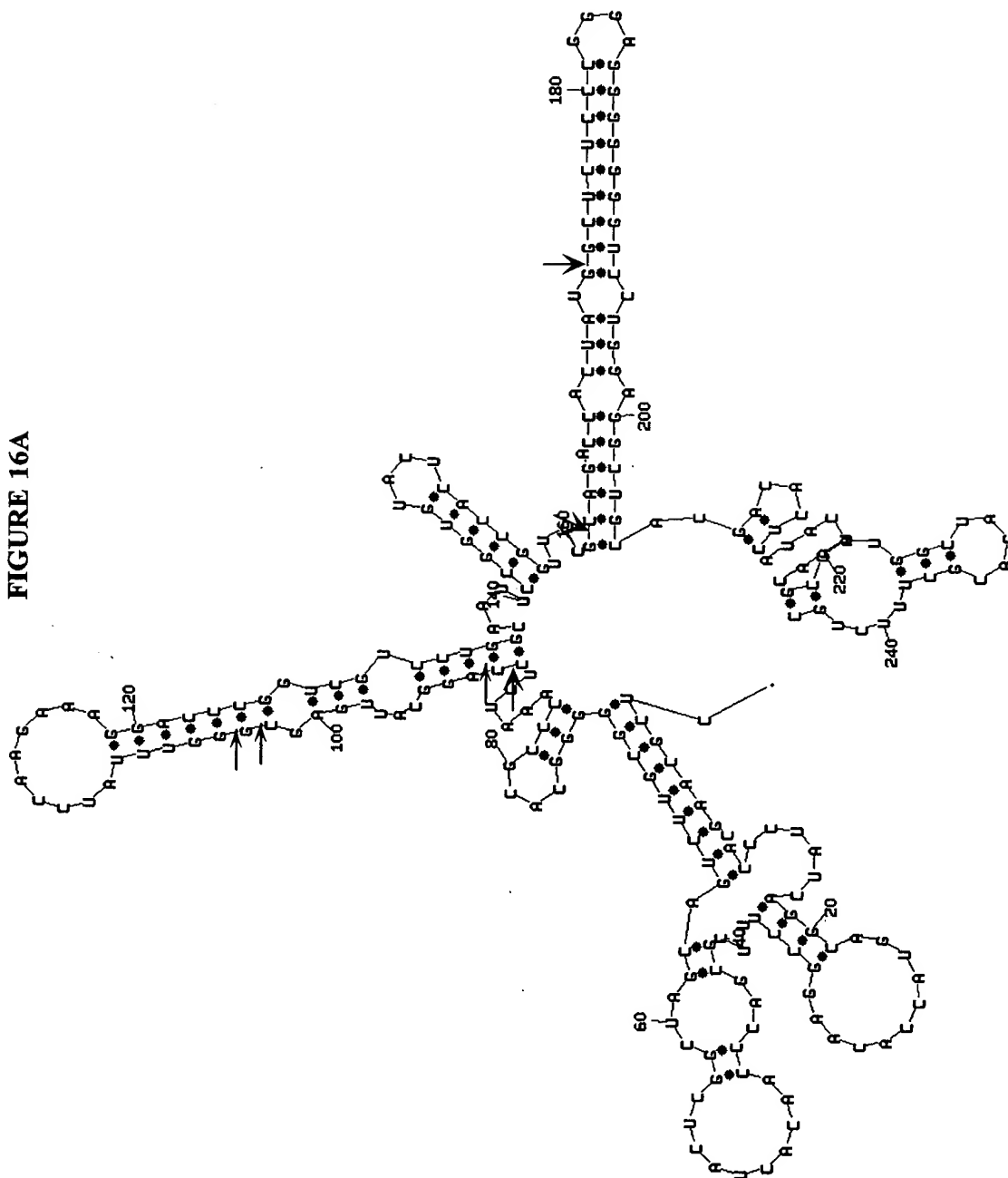


FIGURE 16B

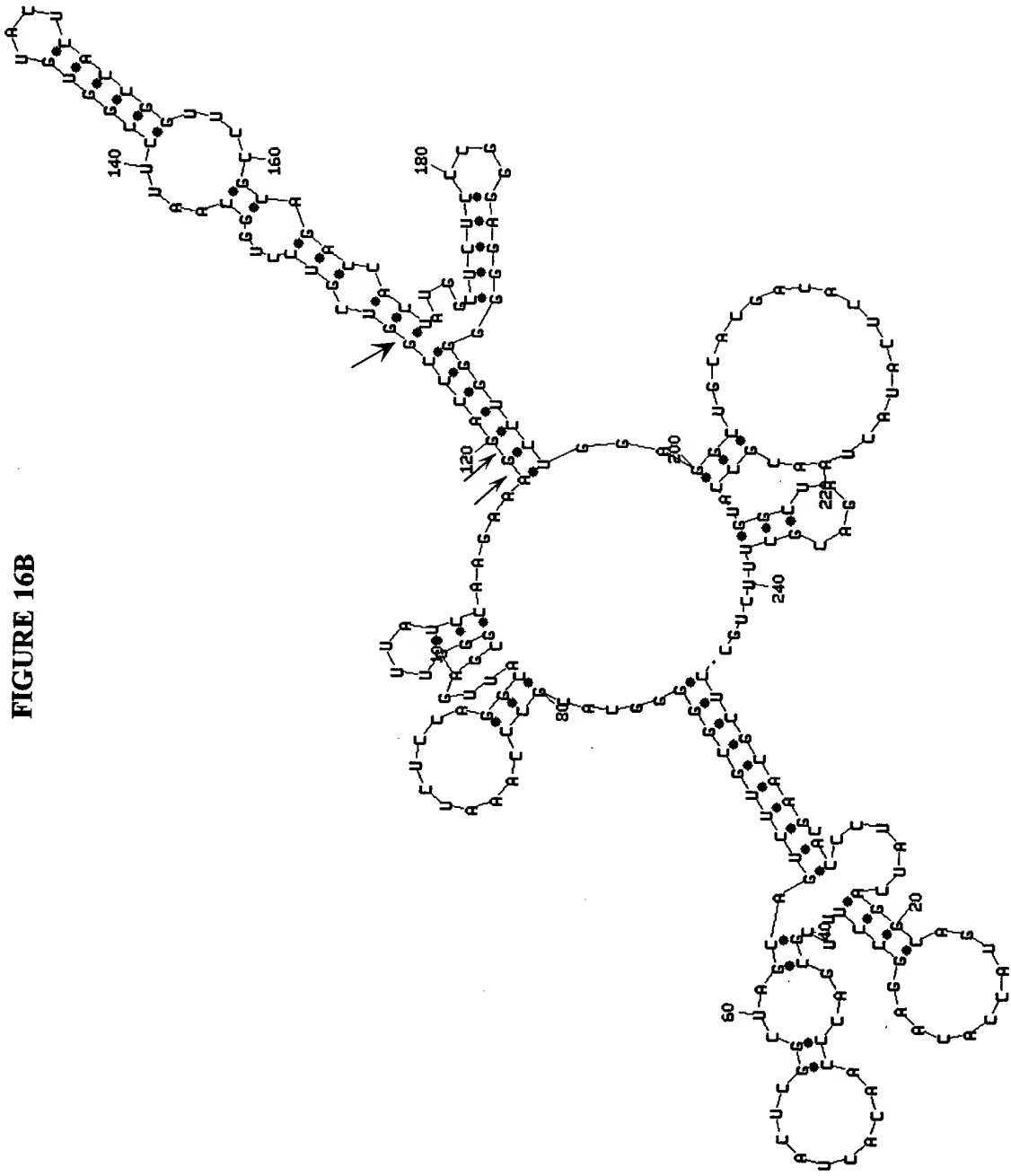


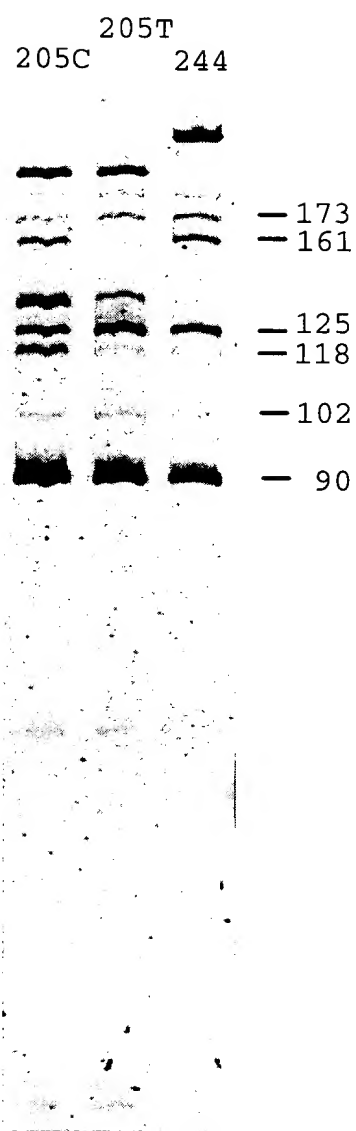
FIGURE 17A

FIGURE 17B

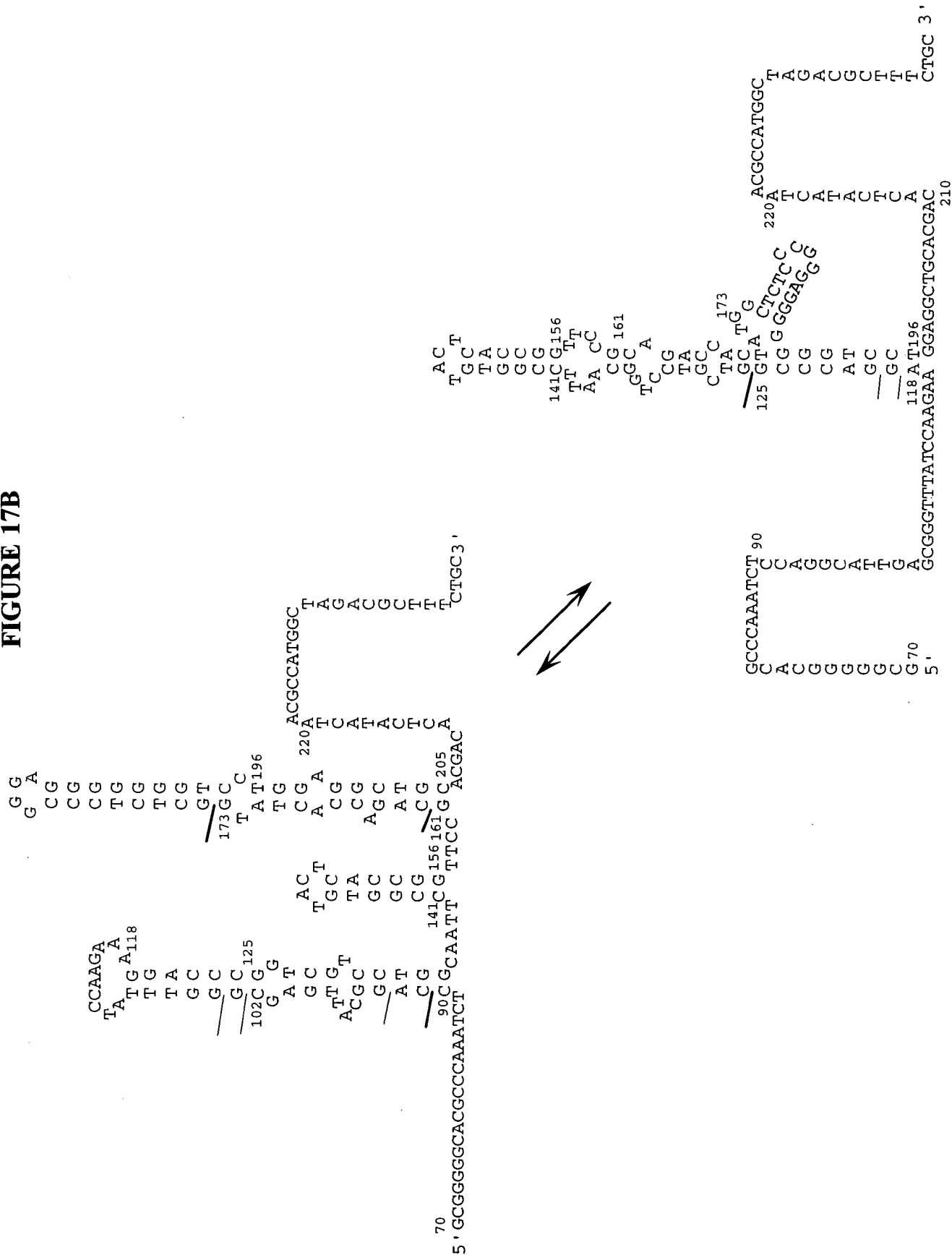


FIGURE 17C



FIGURE 18A

HCV 1a

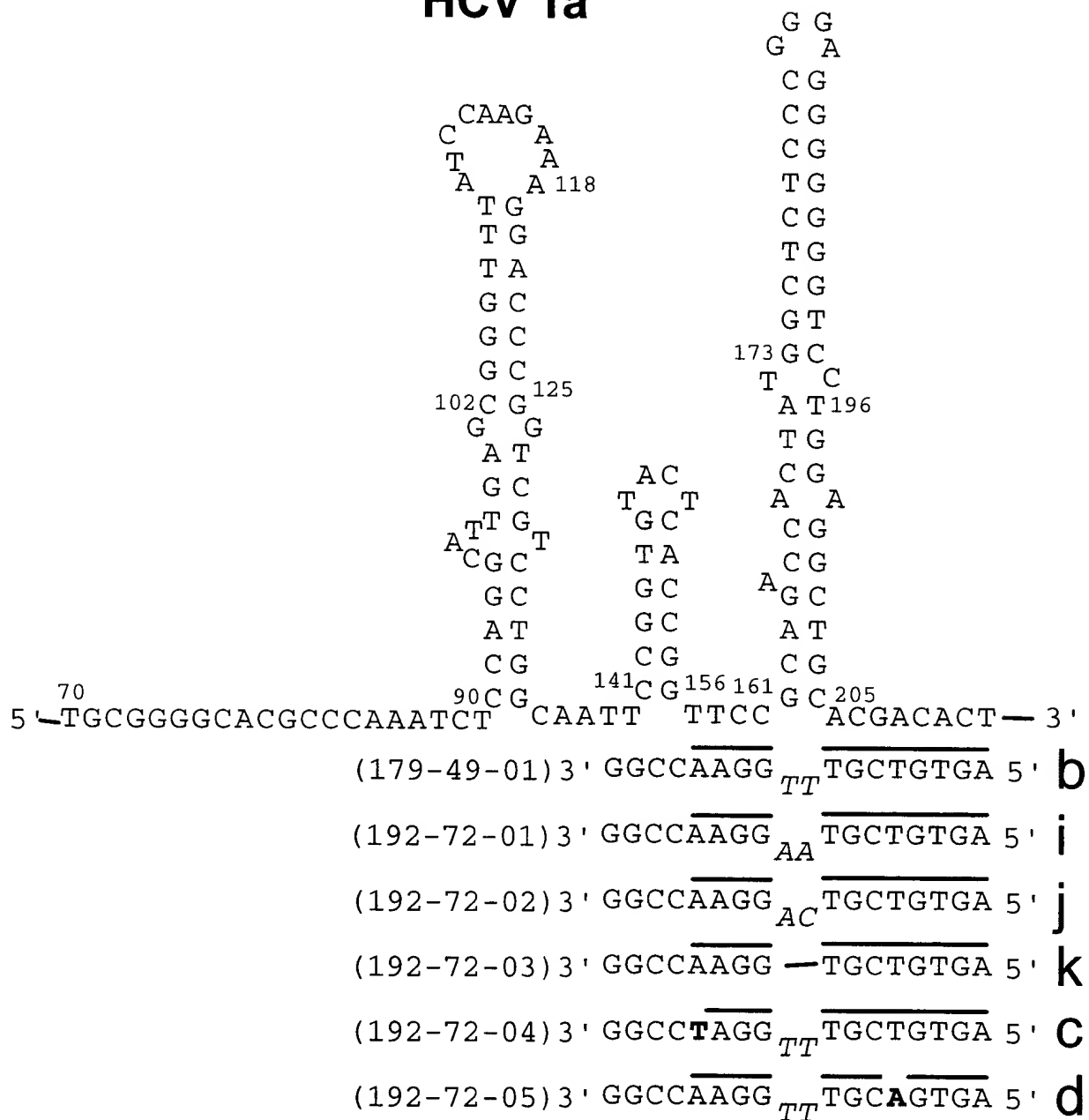


FIGURE 18B

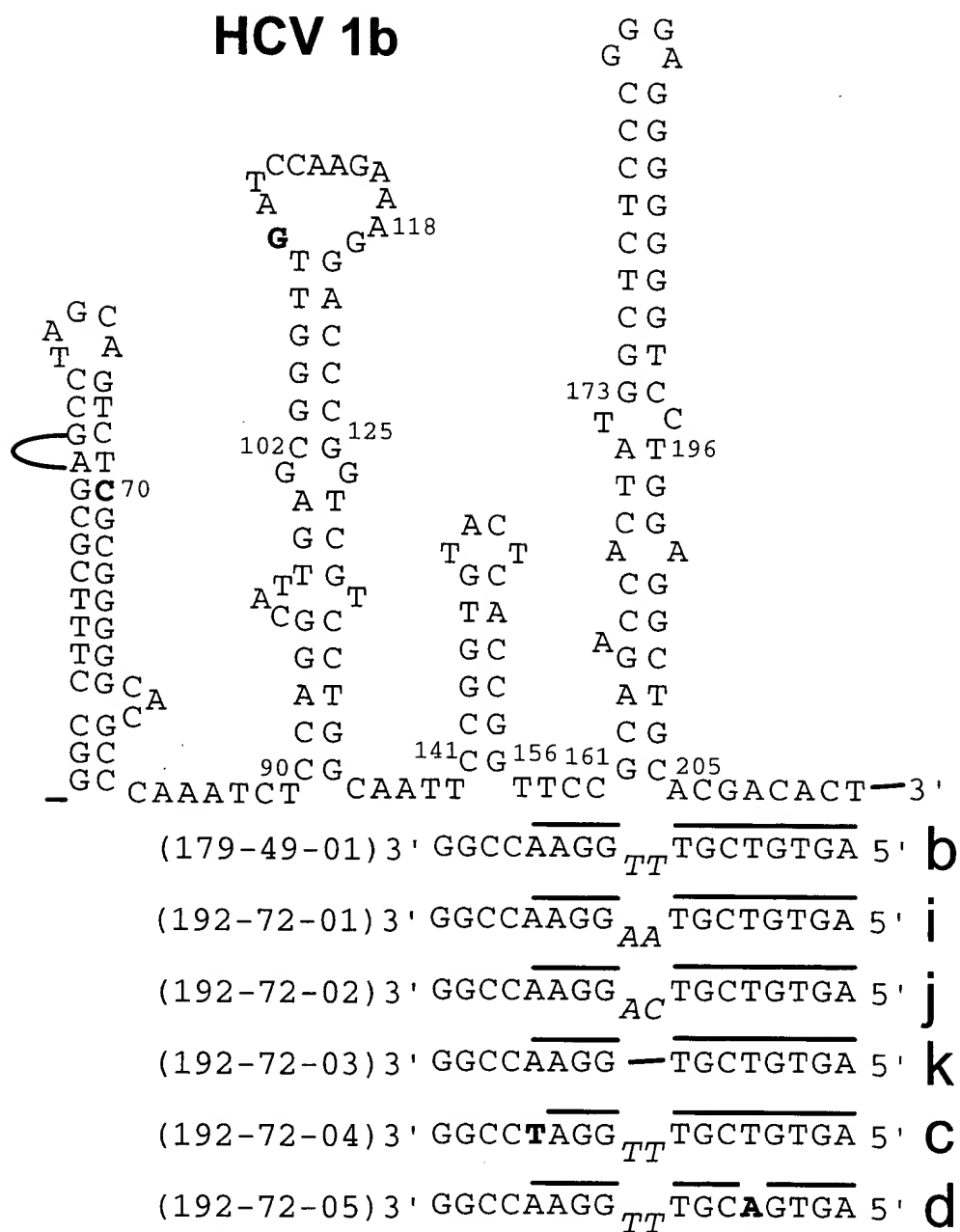


FIGURE 18C

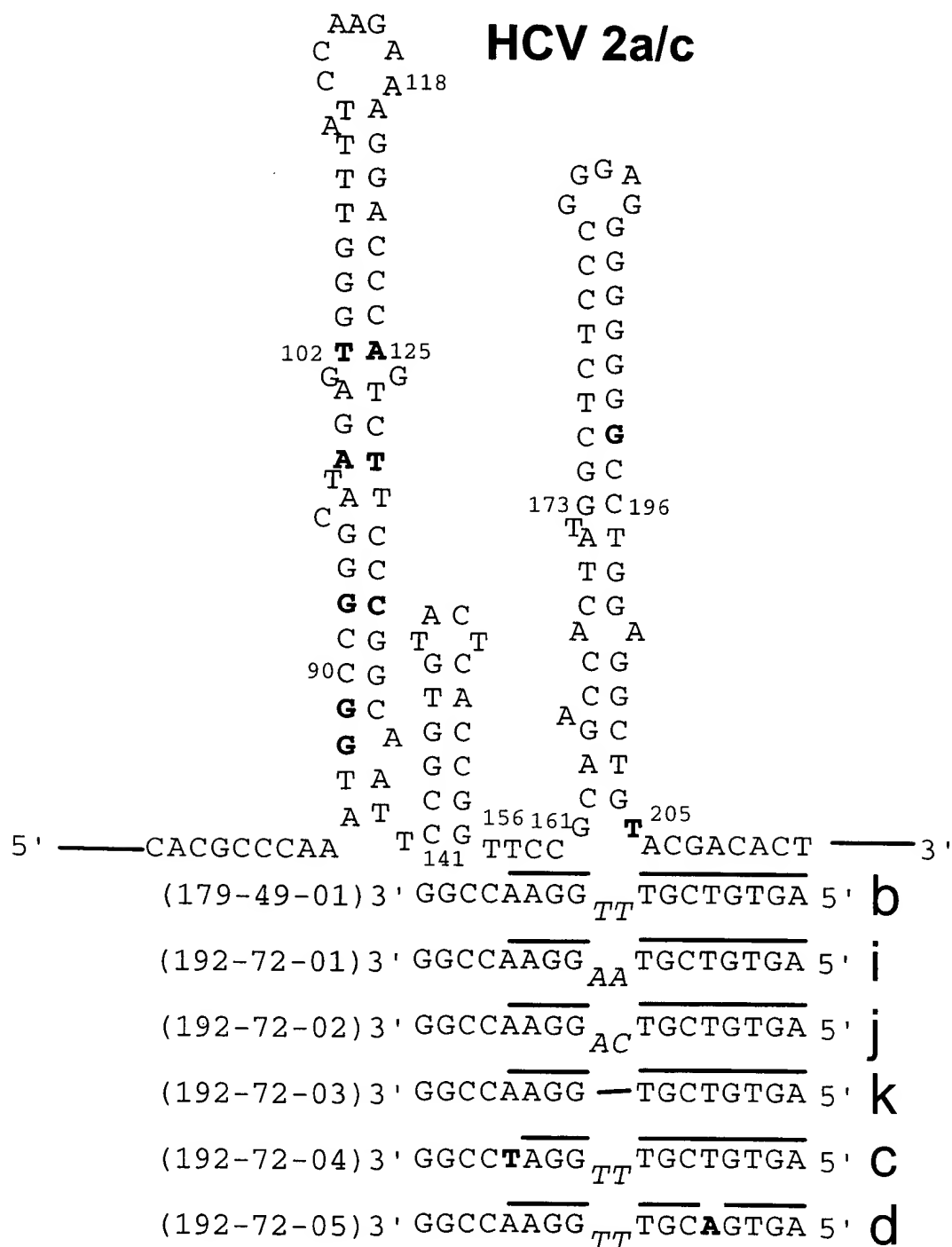


FIGURE 18D

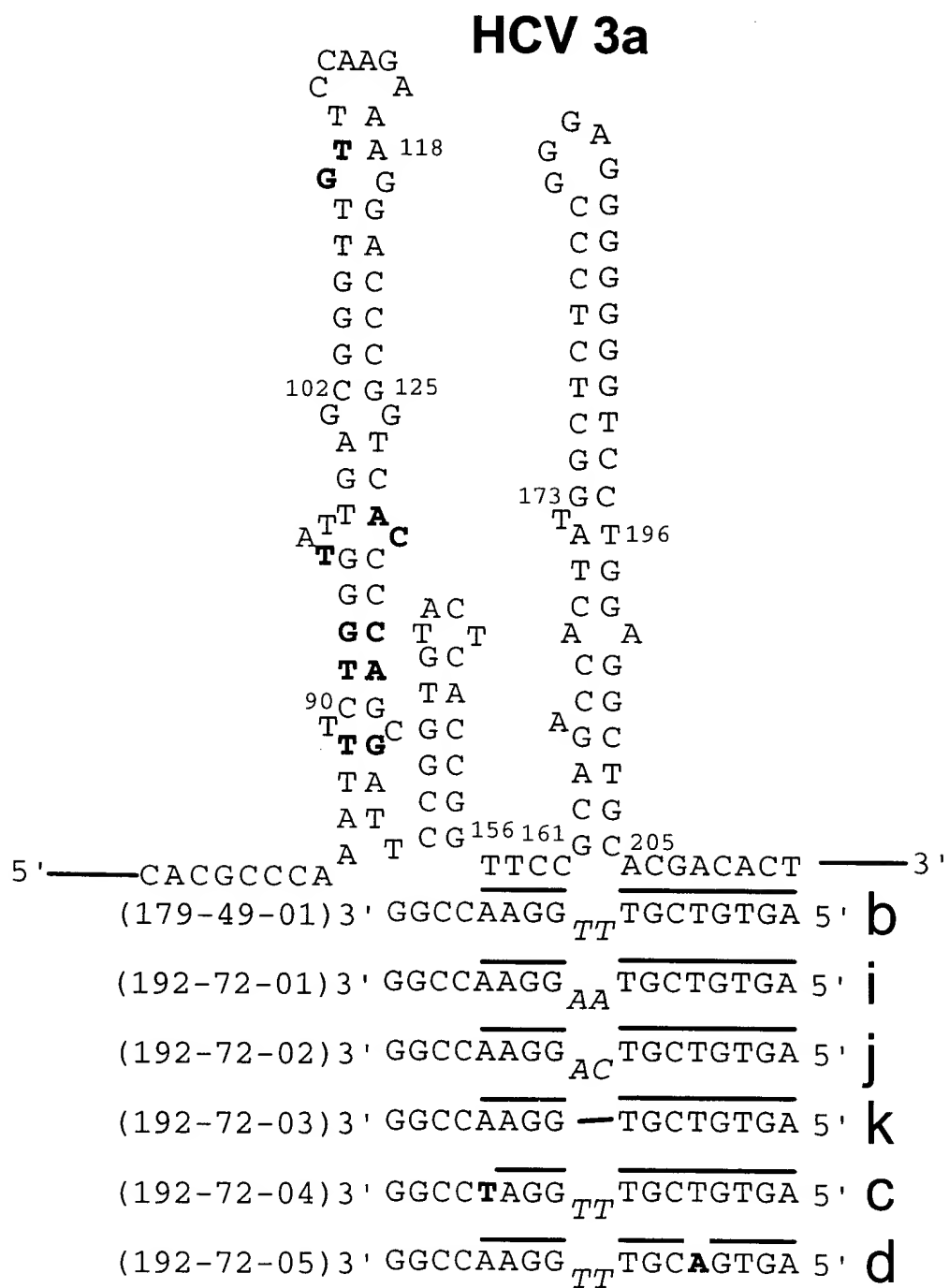


FIGURE 19

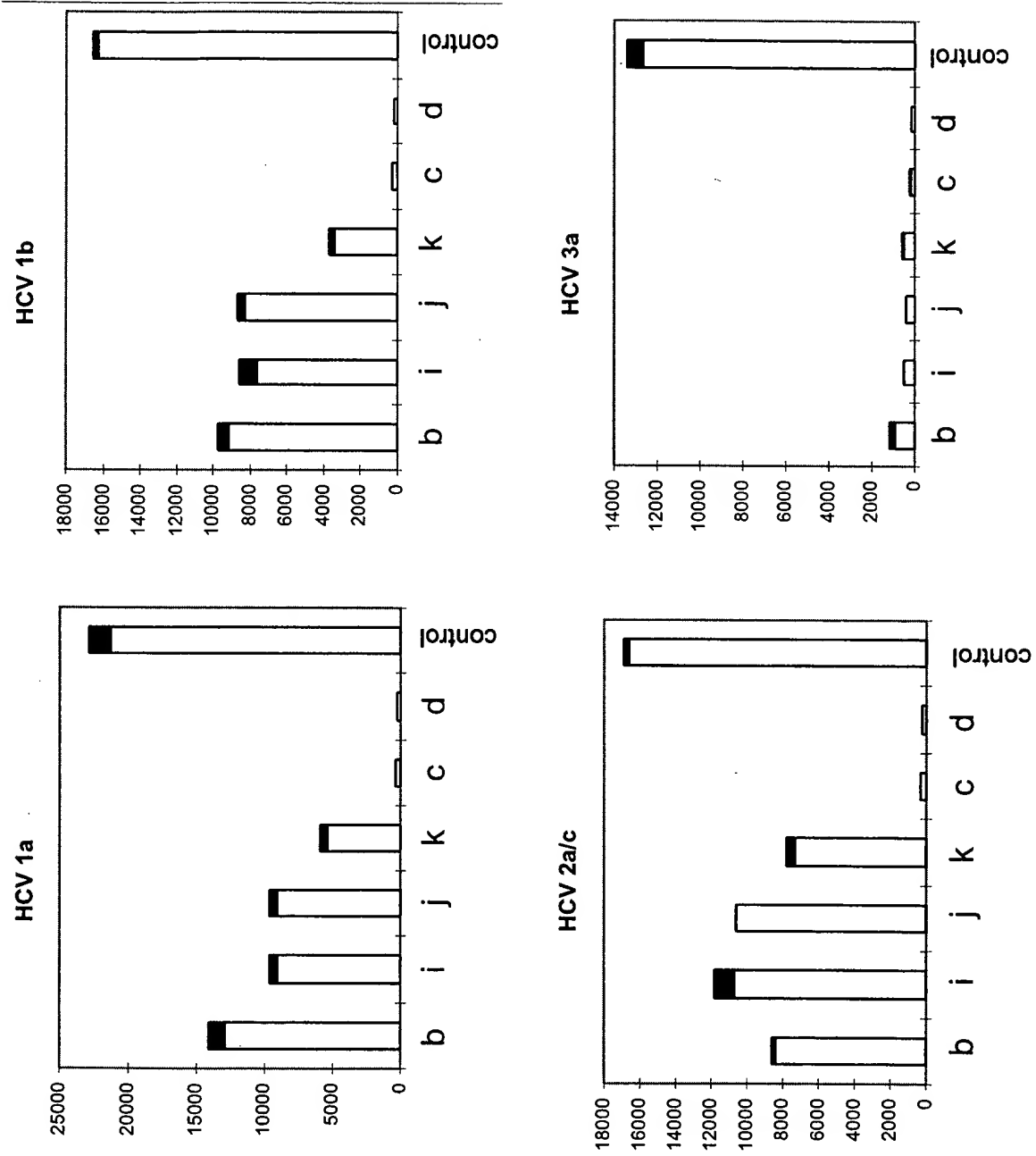


FIGURE 20A

GG
GA
CG
CG
CG
TG
CG
TG
CG
GT
173GGC
TCT
AT196
TG
CG
AA
CG
CG
AGC
AT
CG

HCV 1a

5'-CAATTCCGGTGTA~~CT~~CACCGGTTCCGC²⁰⁵ACGACACT-3'

- 3'-GGCCAAGCGCTCTGGTGA-F1'5' (205-13-02) **a**
- 3'-GGCCAAGG_{TT}TGCTGTGA-F1'5' (179-49-01) **b**
- 3'-GGCC~~T~~AGG_{TT}TGCTGTGA-F1'5' (192-72-04) **c**
- 3'-GGCCAAGG_{TT}TGC~~A~~GTGA-F1'5' (192-72-05) **d**
- 3'-GGCCAAGG-F15' (205-27-01) **e**

FIGURE 20B

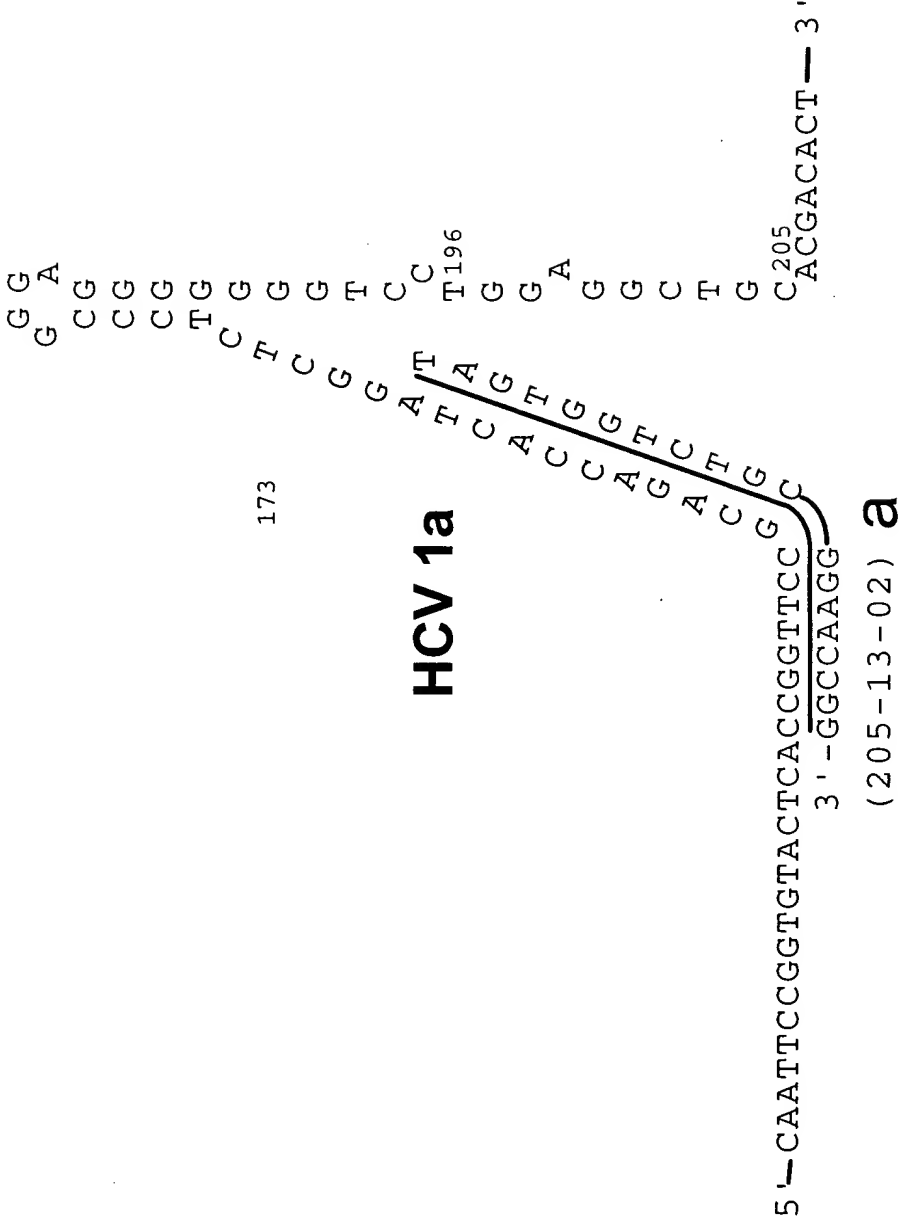


FIGURE 21

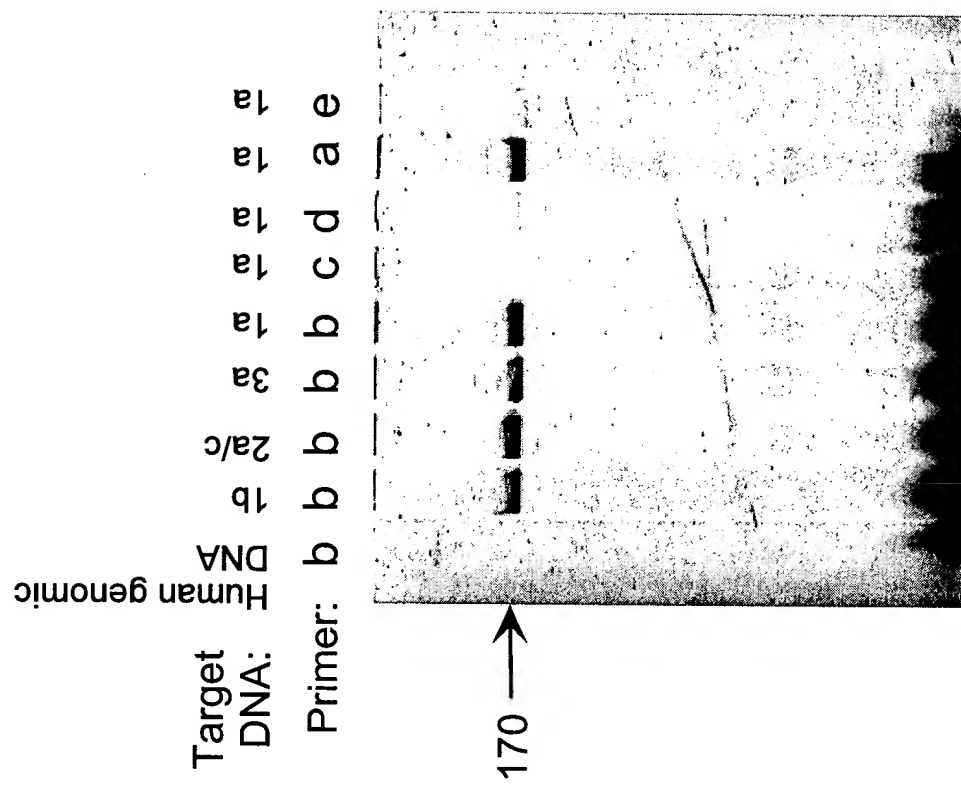


FIGURE 22

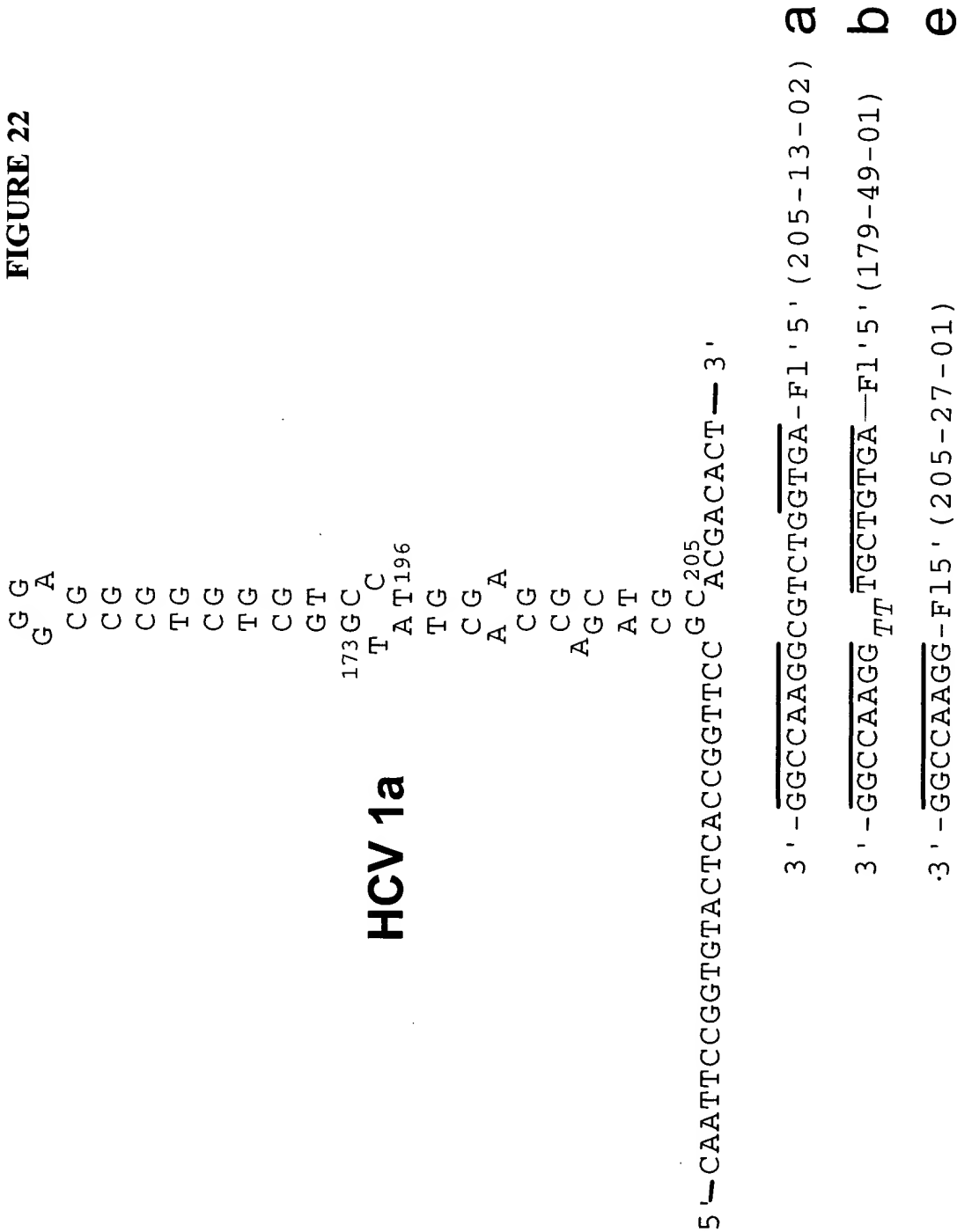


FIGURE 23

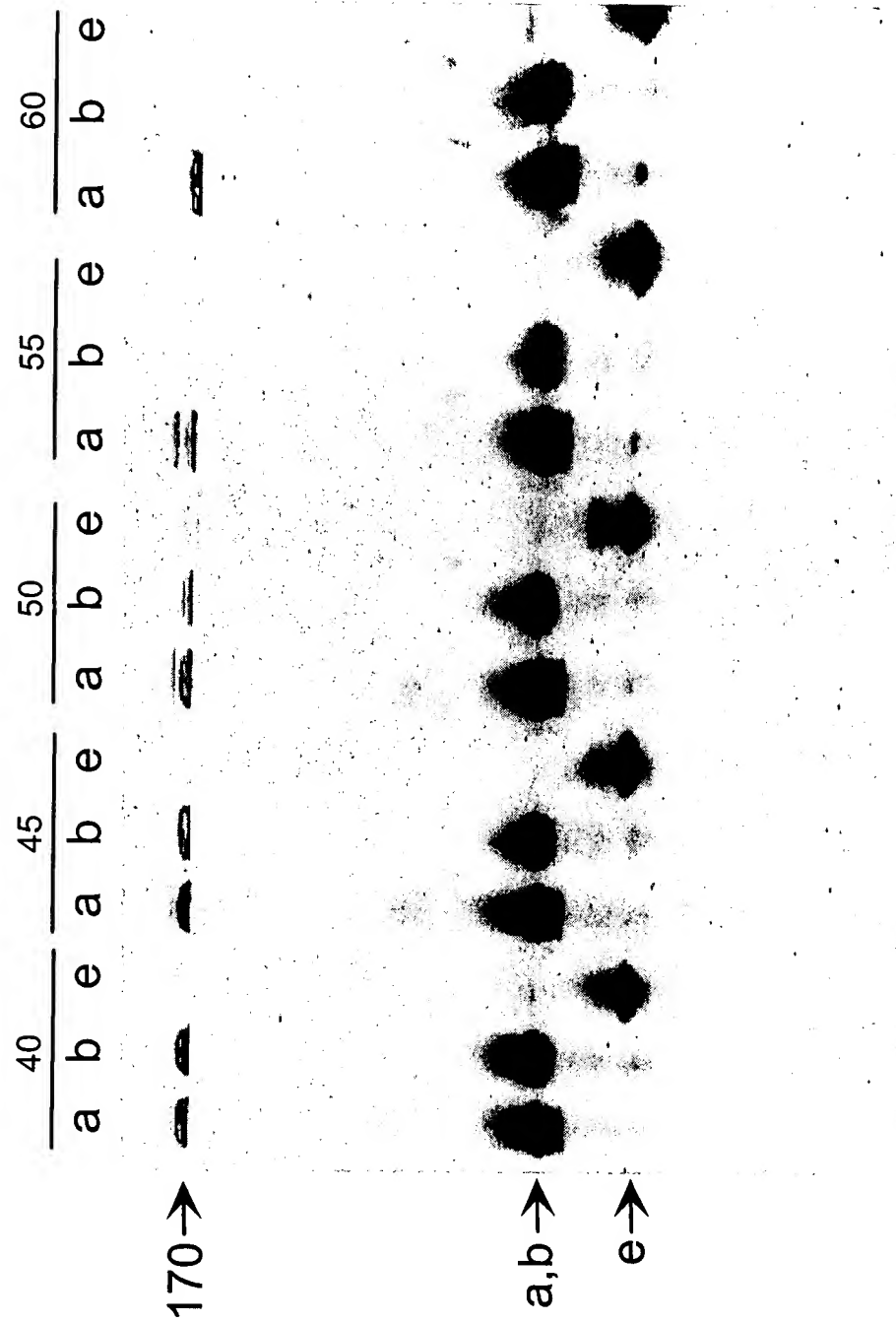


FIGURE 24

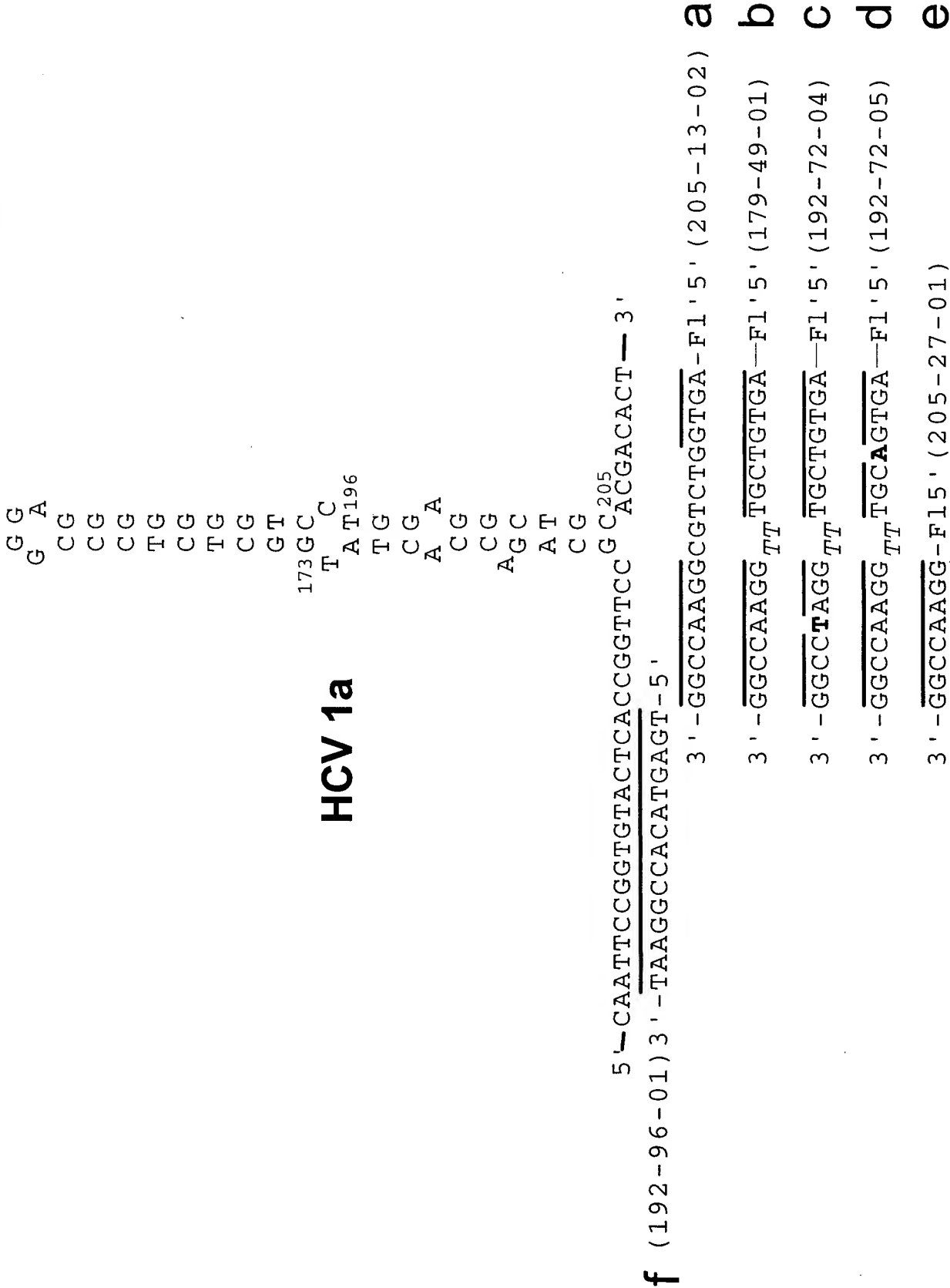


FIGURE 25

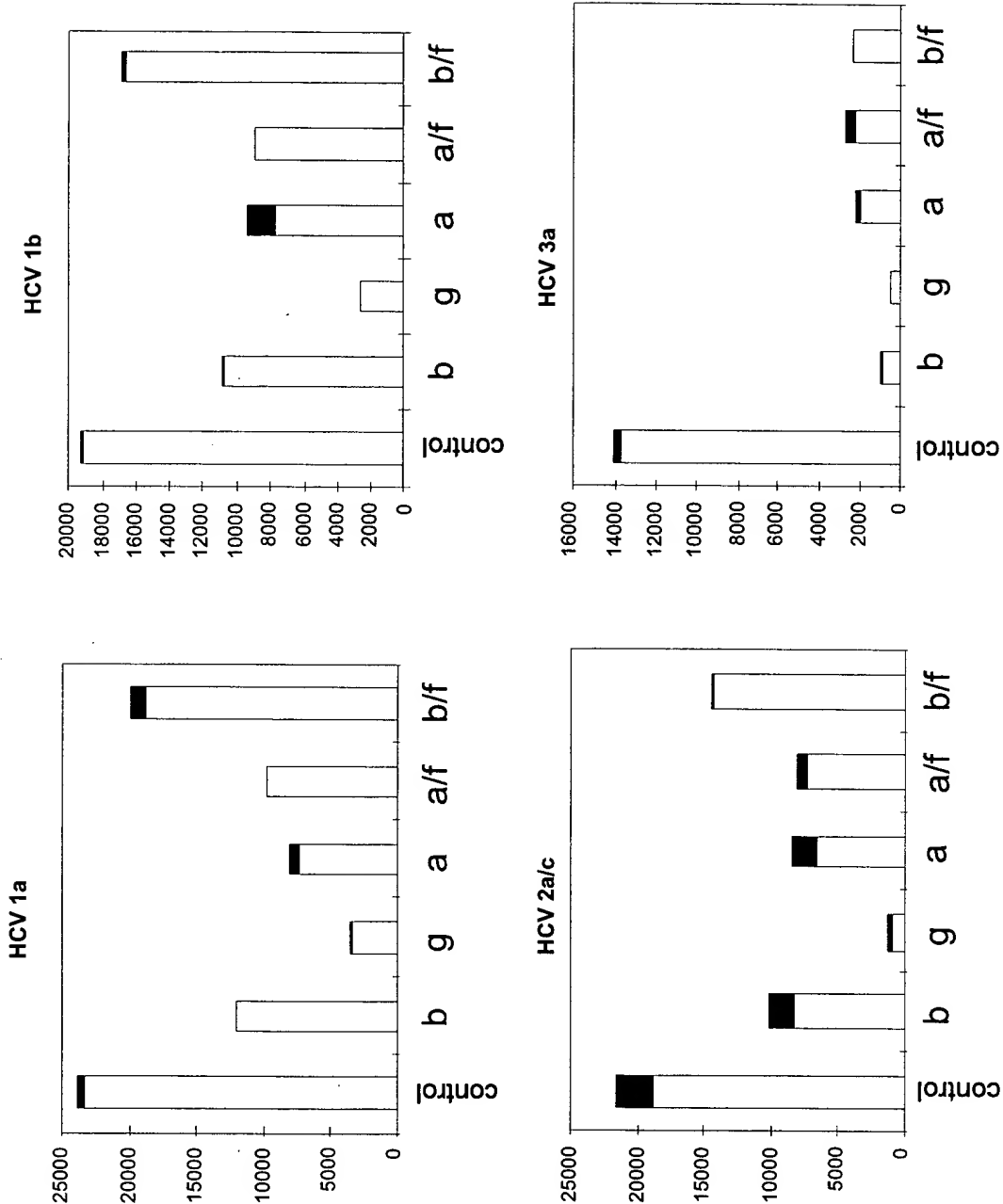


FIGURE 26

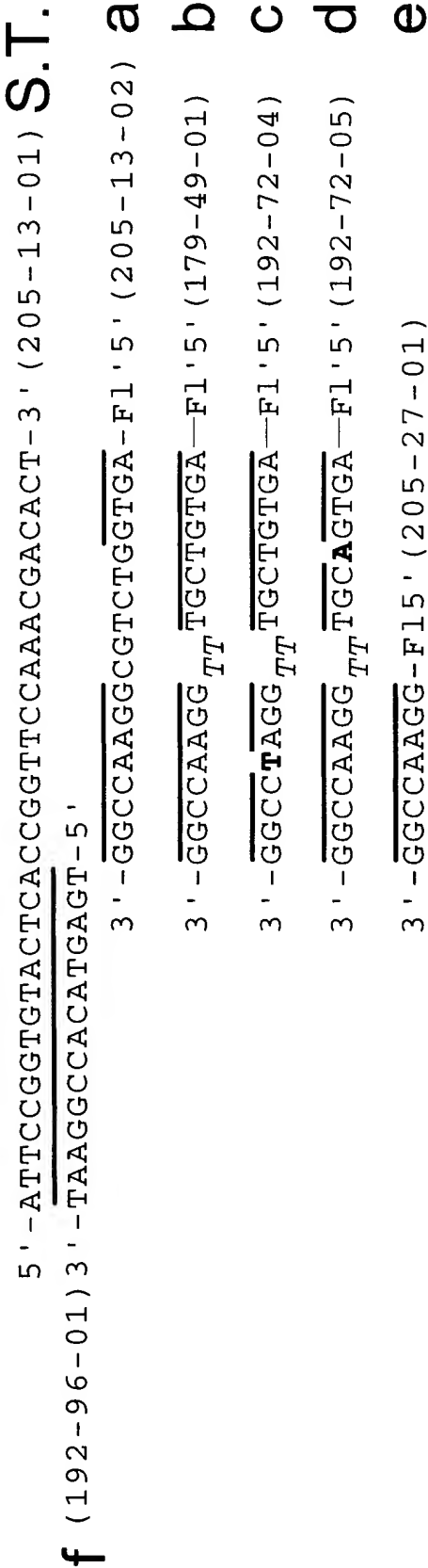


FIGURE 27

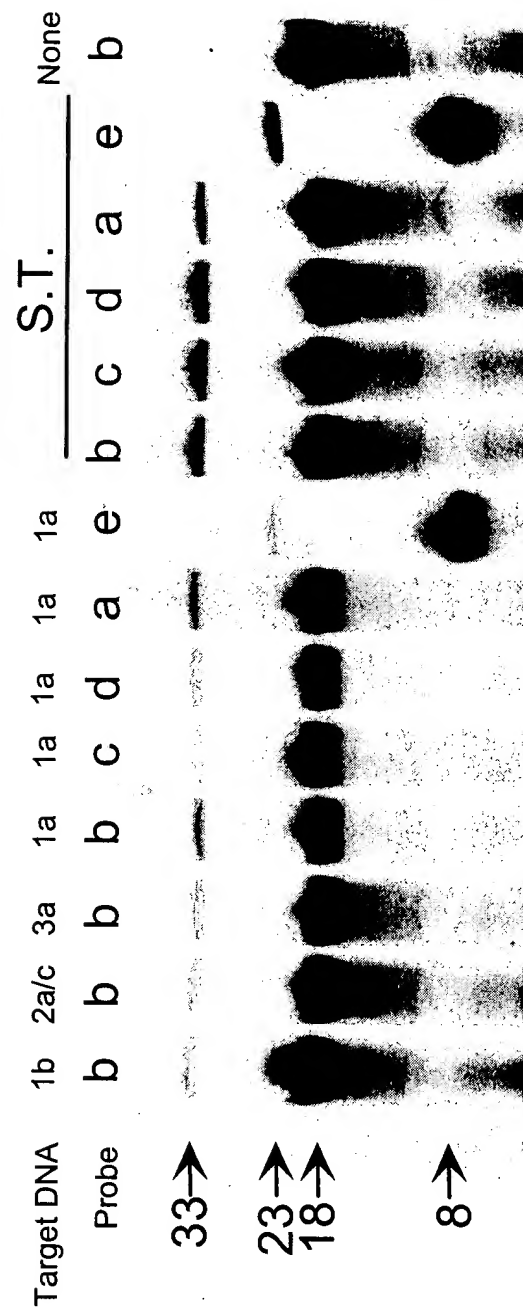
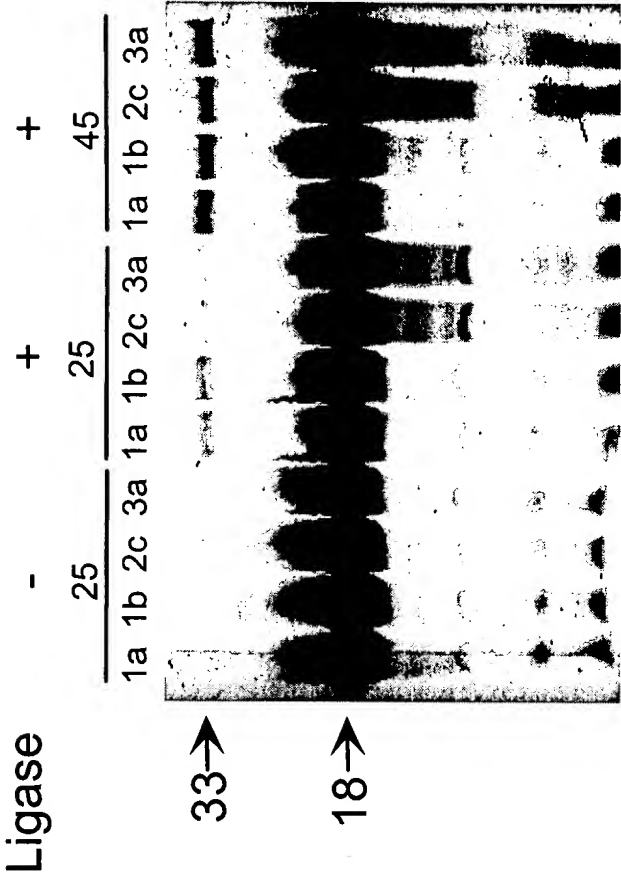


FIGURE 28



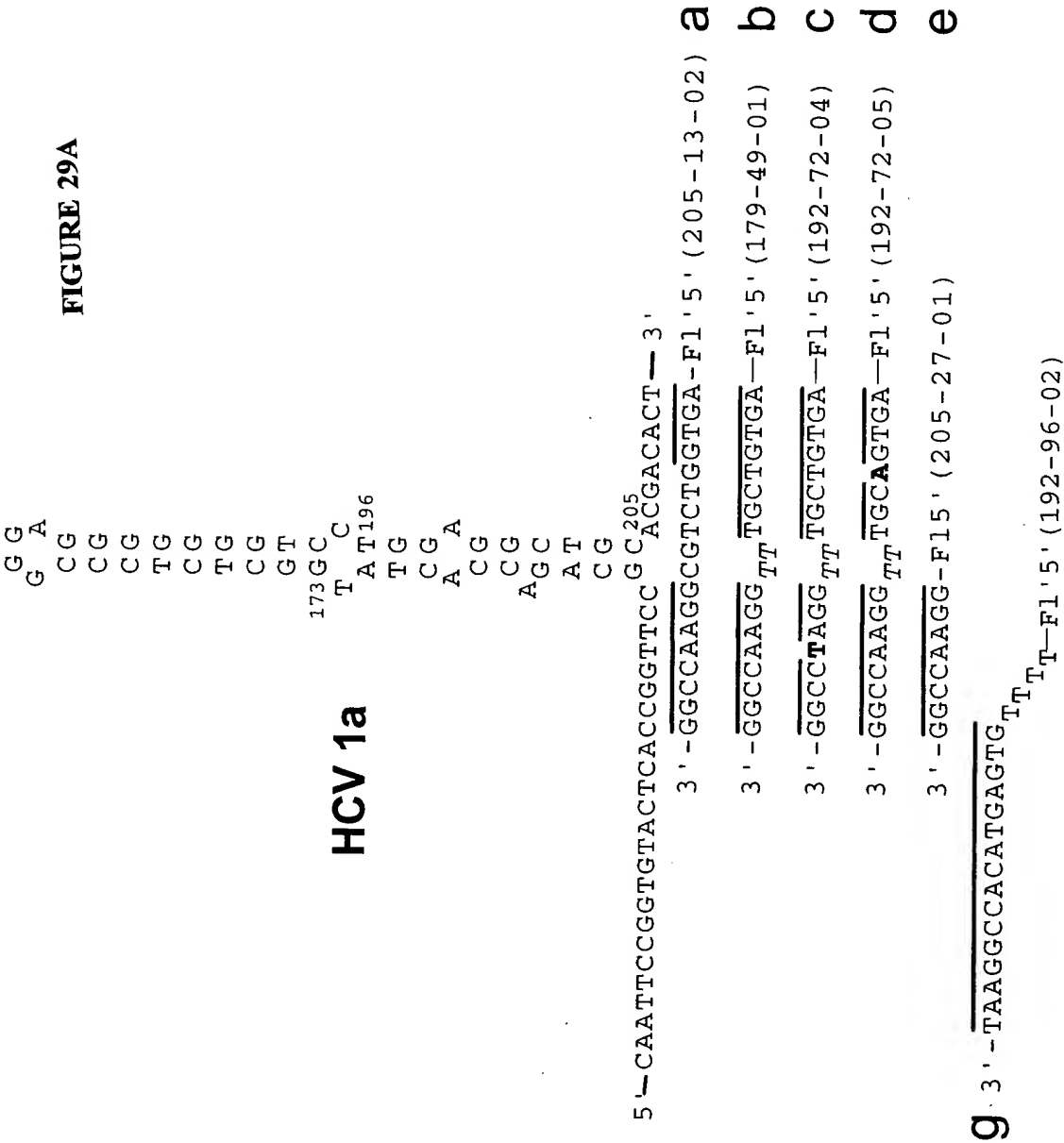


FIGURE 29B

5' -ATCCGGTGTA CTACCGGTCCAAACGACACT-3' (205-13-01) **S.T.**

3' -GGCCAAAGCGTCTGGTGA-F1'5' (205-13-02) **a**

3' -GGCCAAAGG_{T_T}TGCTGTGA-F1'5' (179-49-01) **b**

3' -GGCC**T**AGG_{T_T}TGCTGTGA-F1'5' (192-72-04) **c**

3' -GGCCAAAGG_{T_T}TGC**A**GTGA-F1'5' (192-72-05) **d**

3' -GGCCAAAGG-F15' (205-27-01) **e**

g 3' -TAAGGCCACATGAGTG_{T_T}_{T_T}-F1'5' (192-96-02)

FIGURE 31

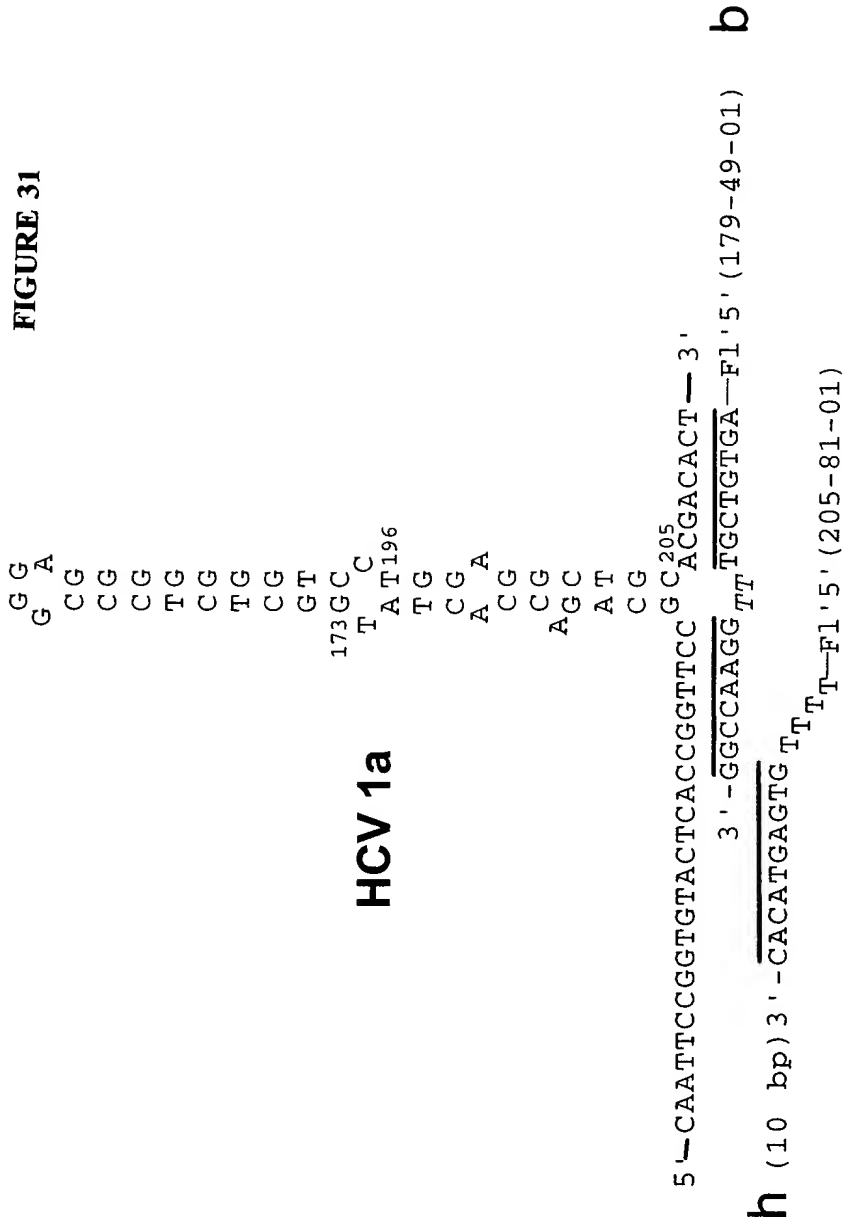


FIGURE 32

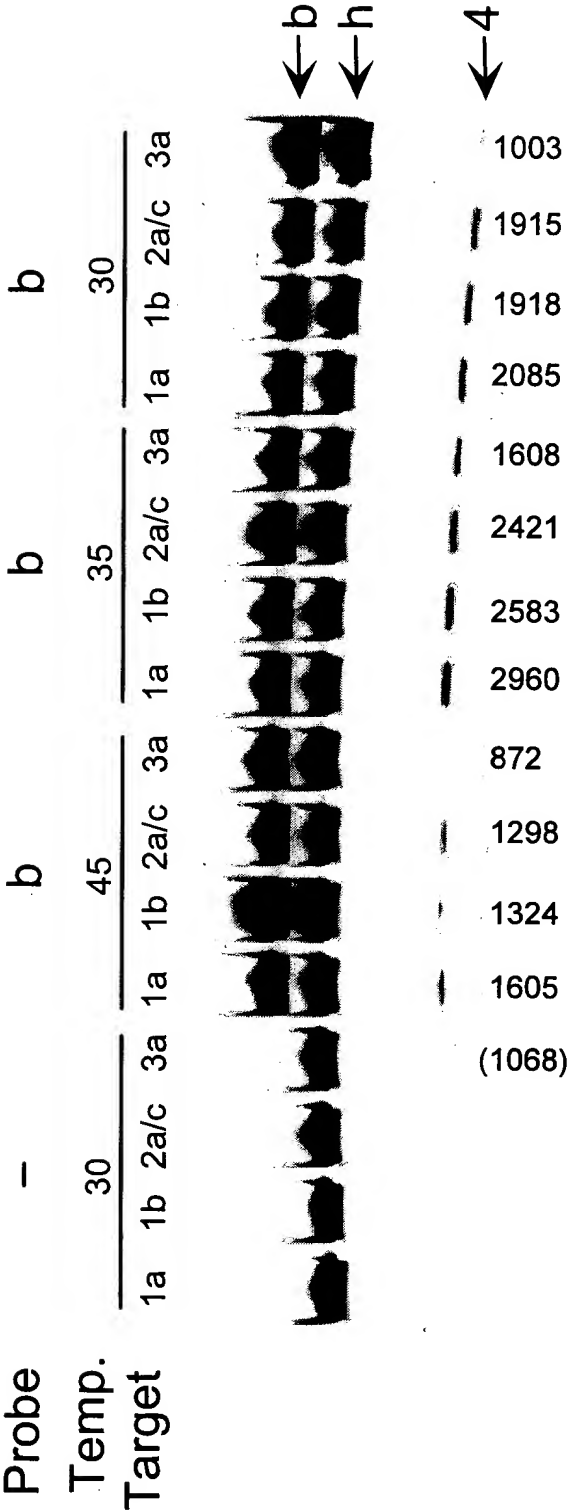


FIGURE 34

STEPS

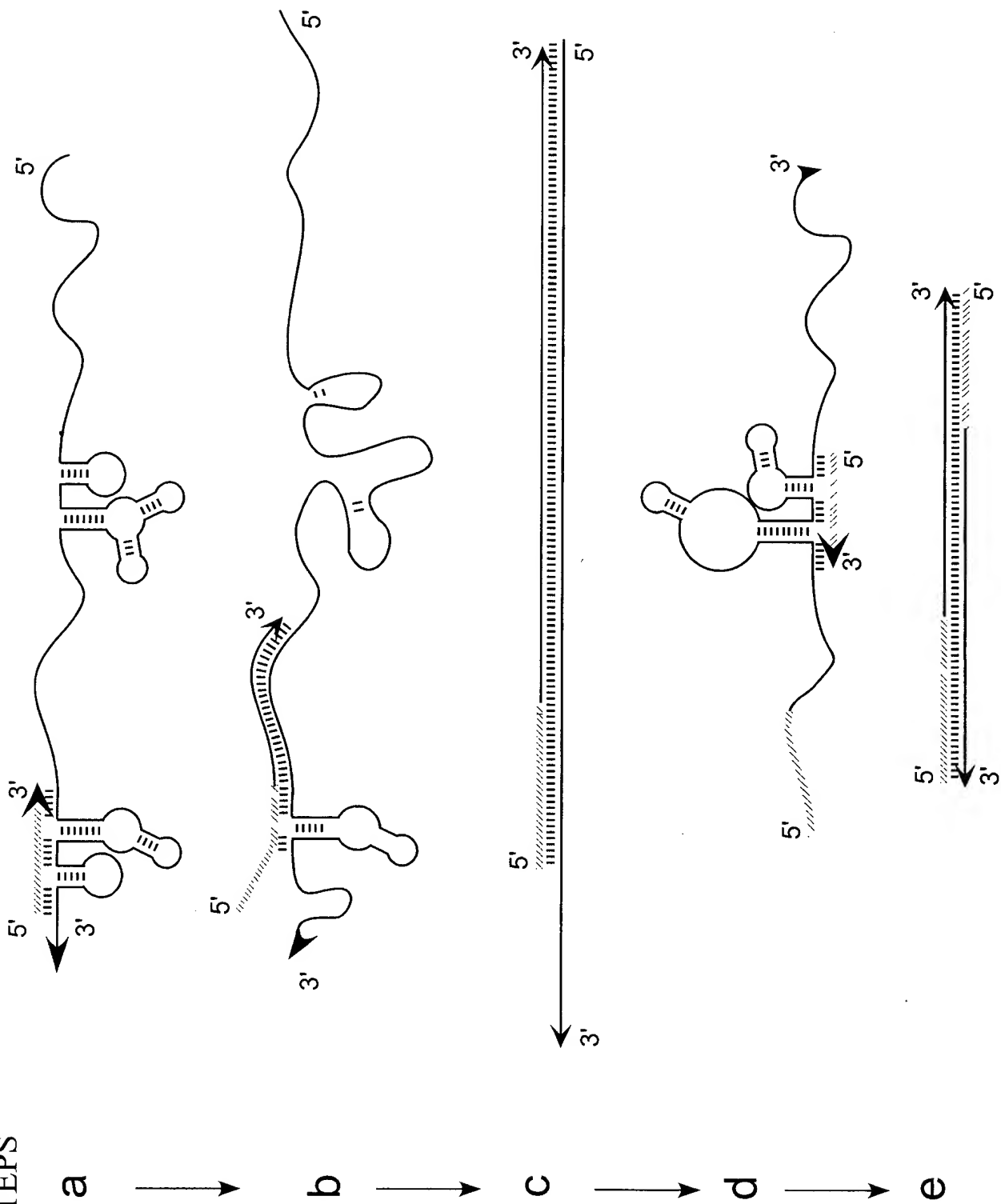


FIGURE 36

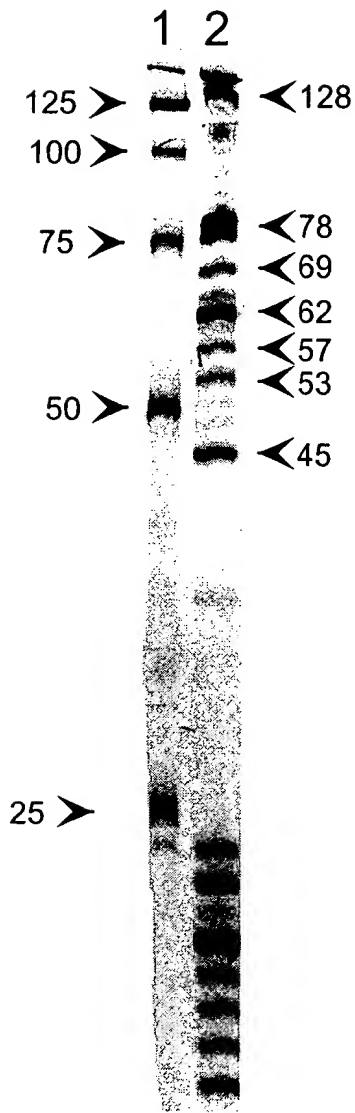
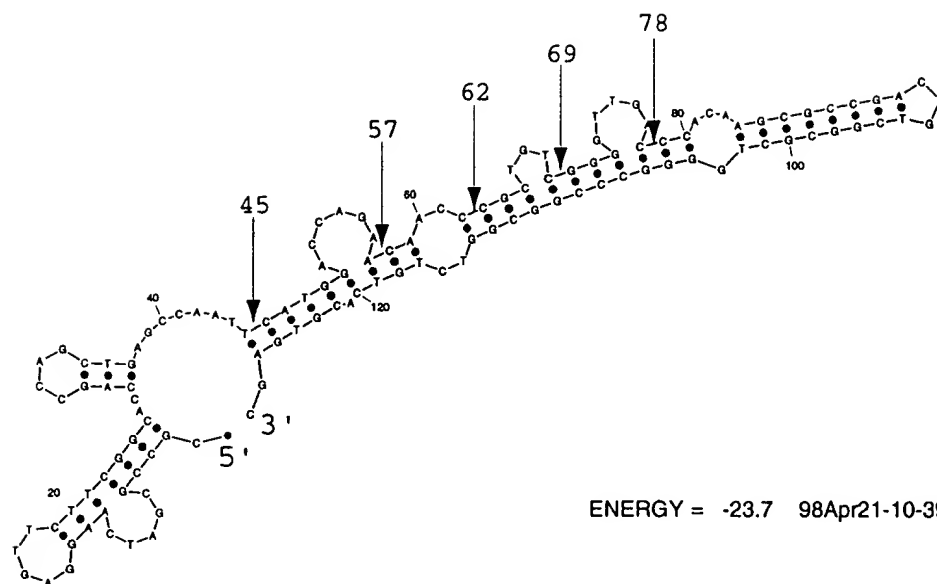
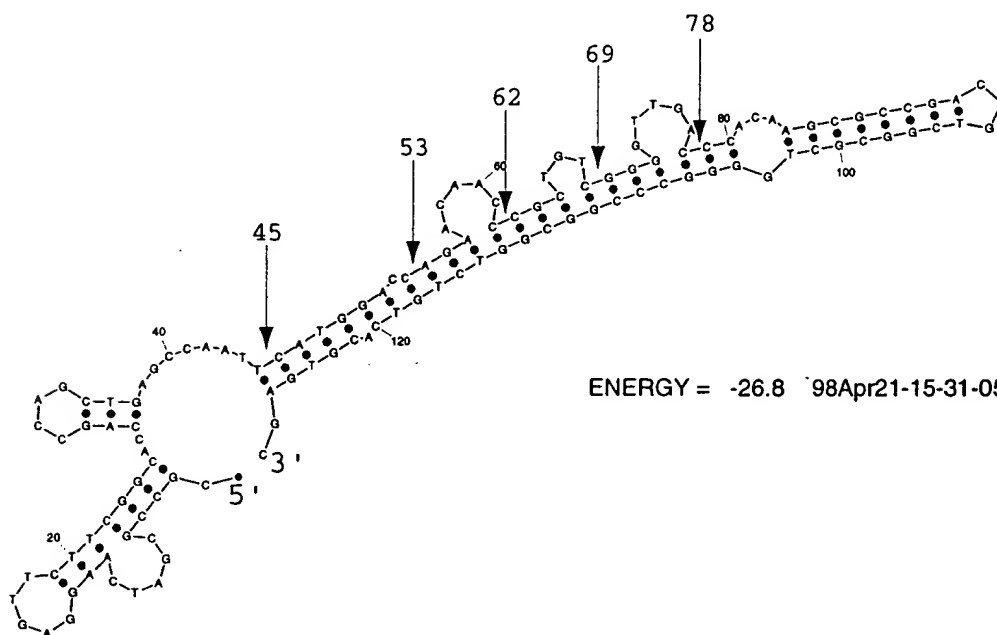


FIGURE 37A



ENERGY = -23.7 98Apr21-10-39-54



ENERGY = -26.8 98Apr21-15-31-05

FIGURE 37B

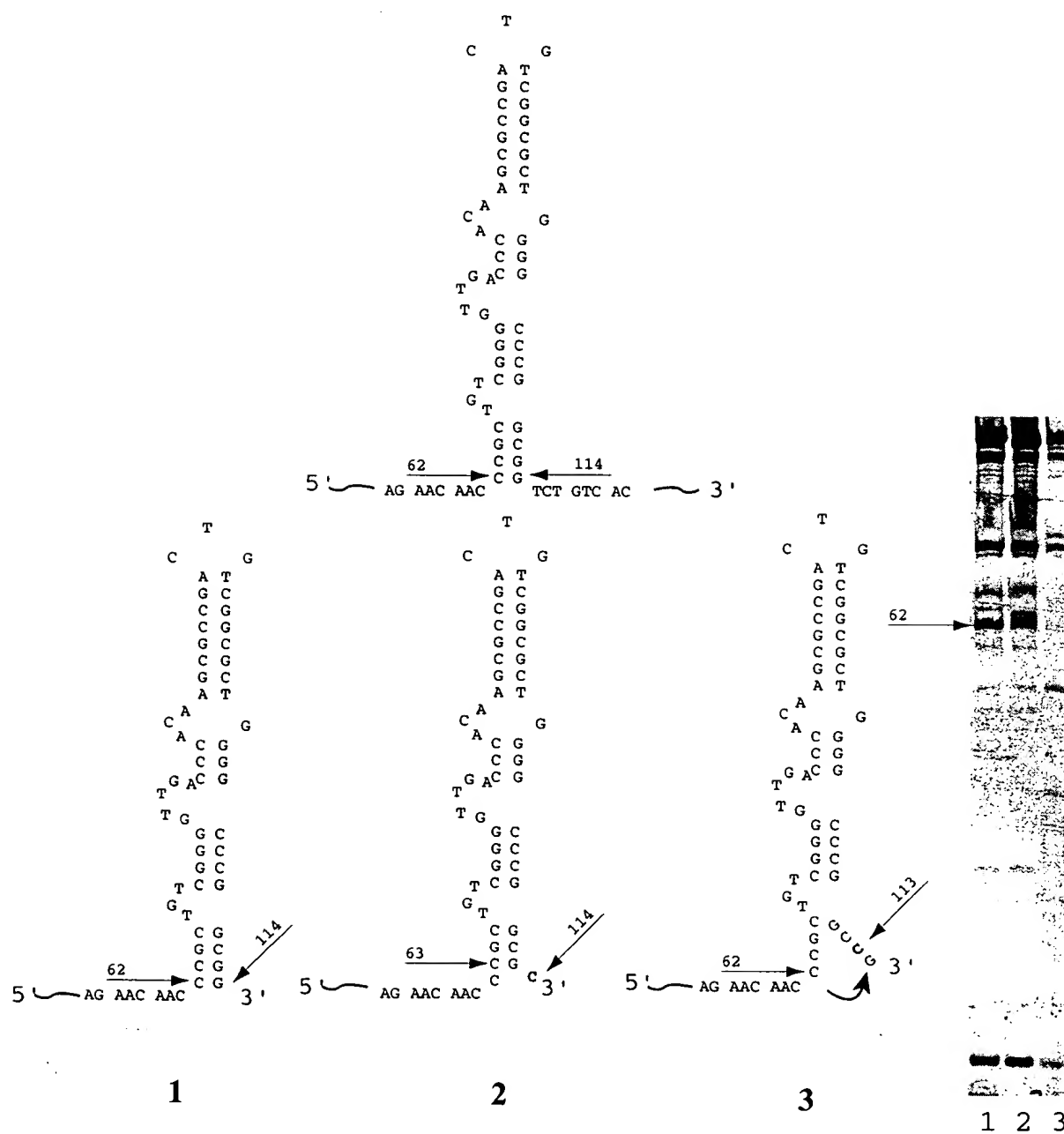


FIGURE 37C

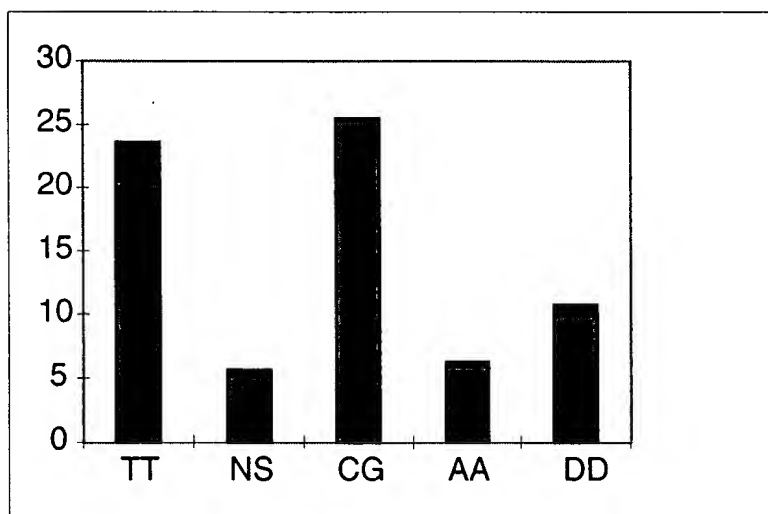
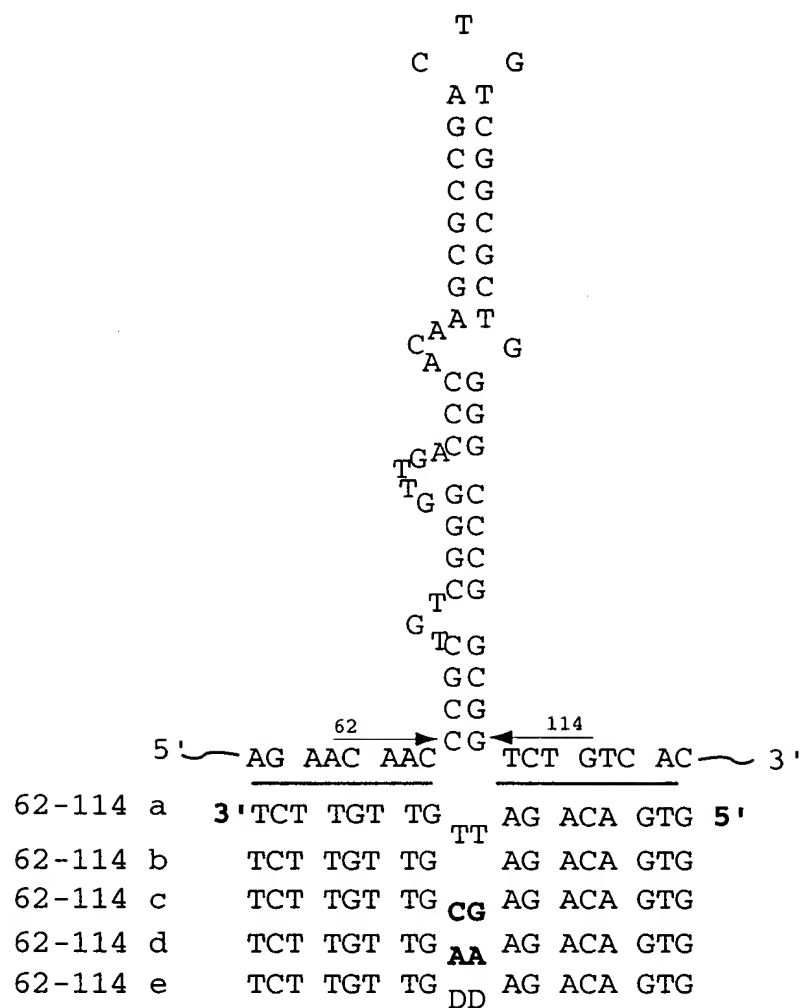


FIGURE 38A

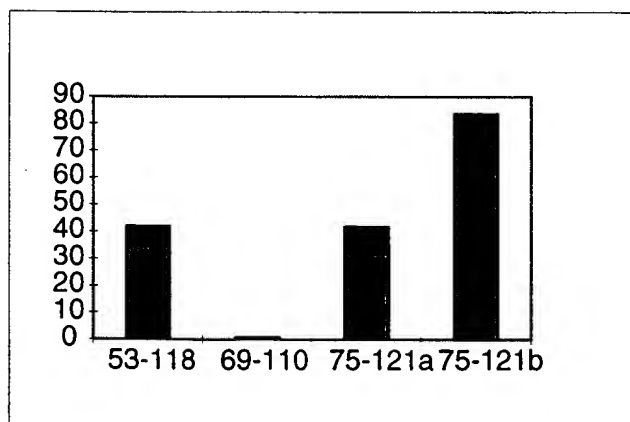
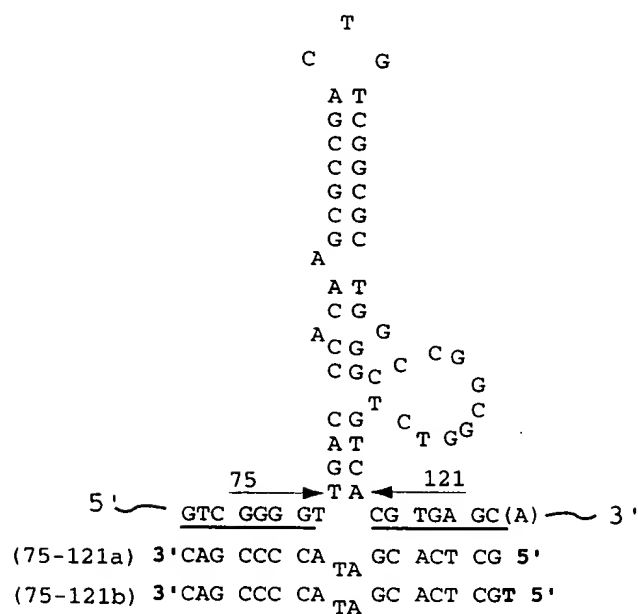
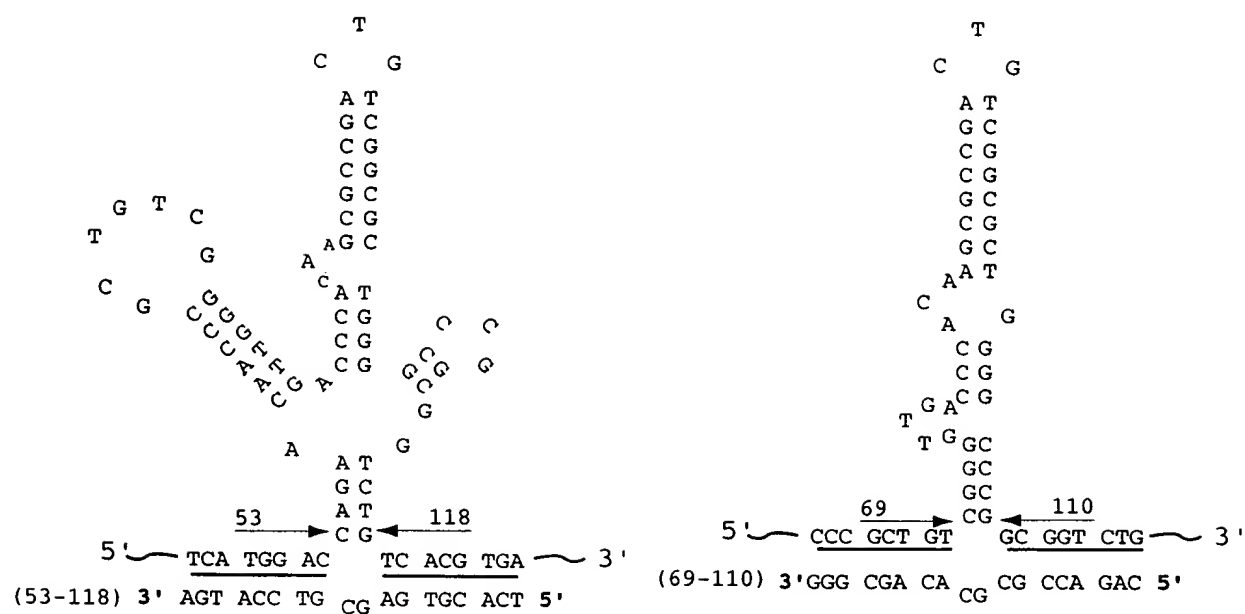


FIGURE 38B

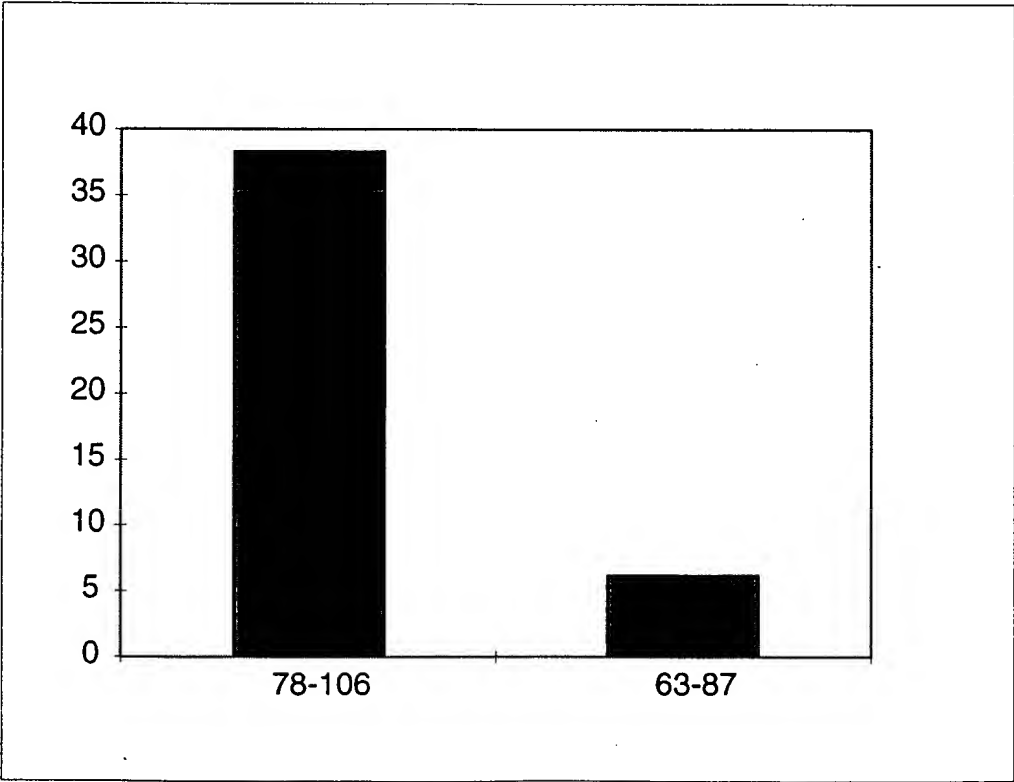
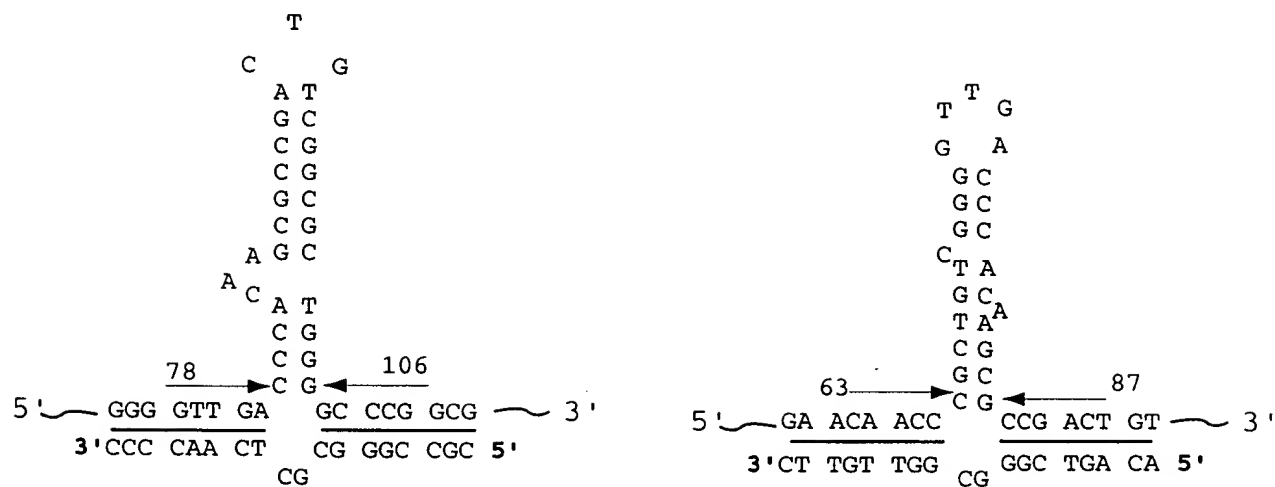


FIGURE 38C

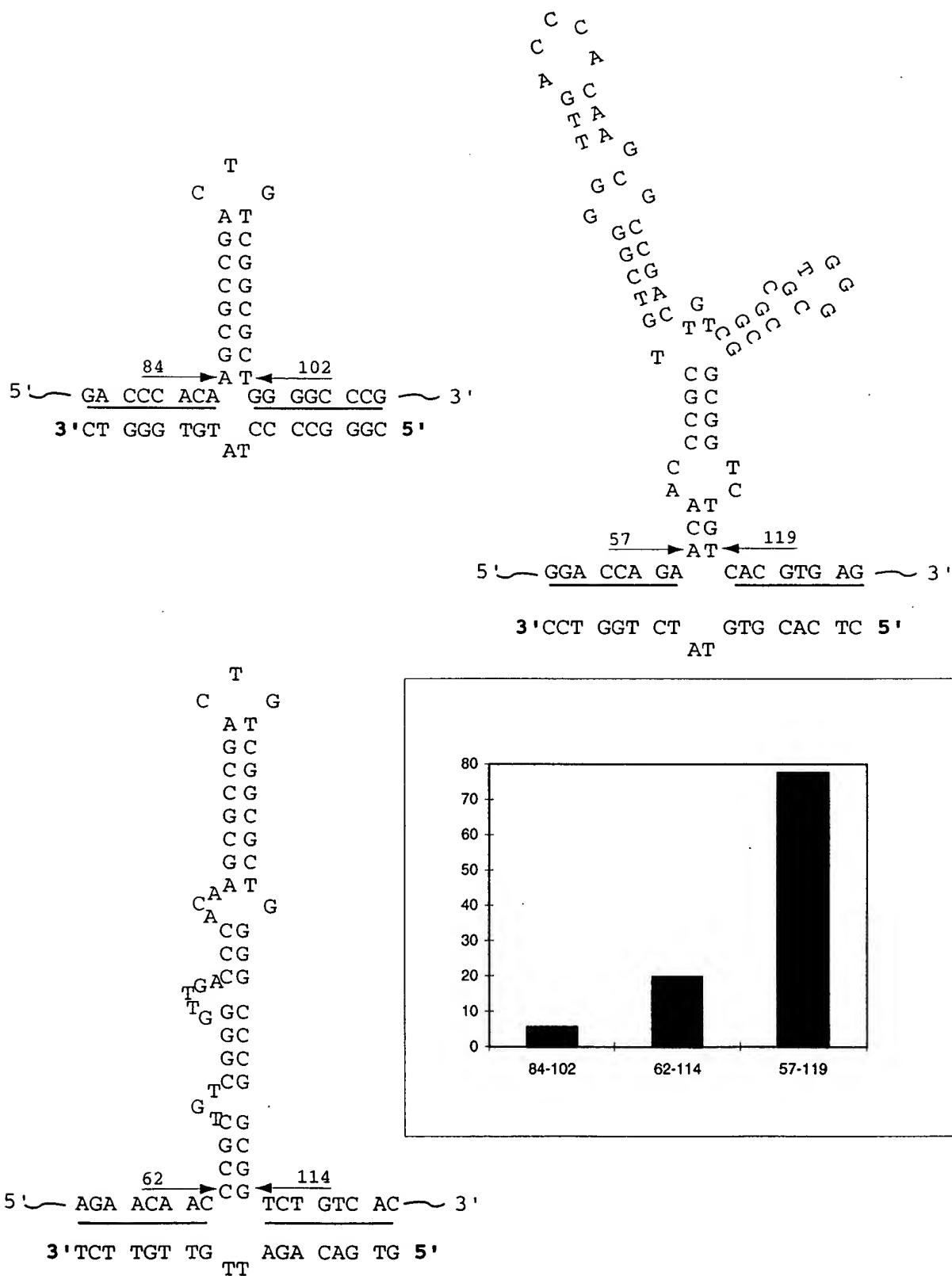


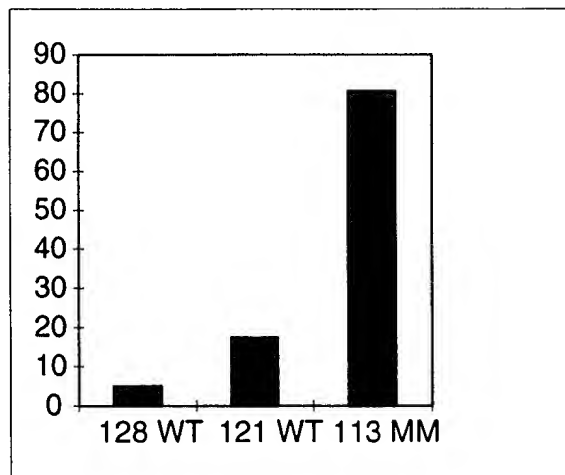
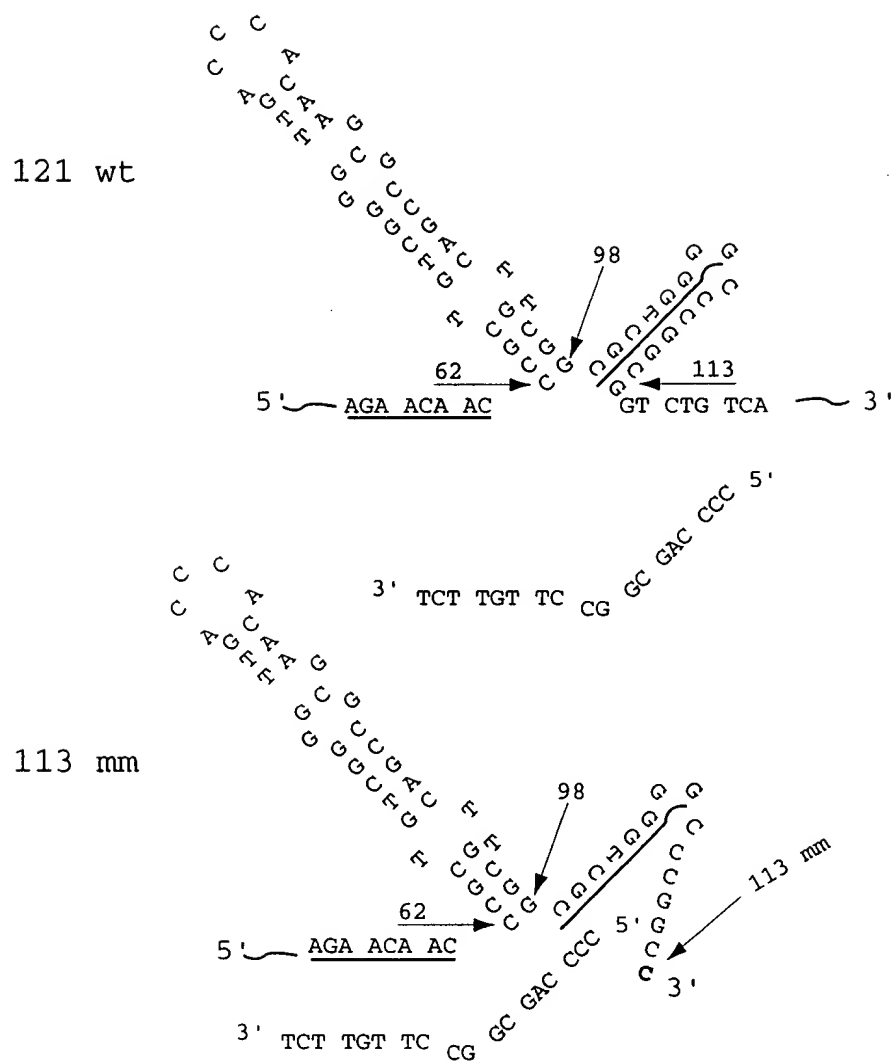
FIGURE 41

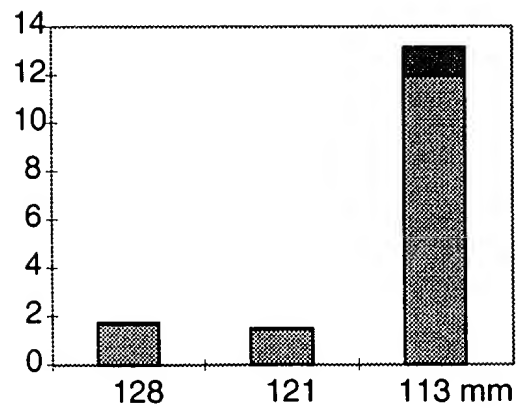
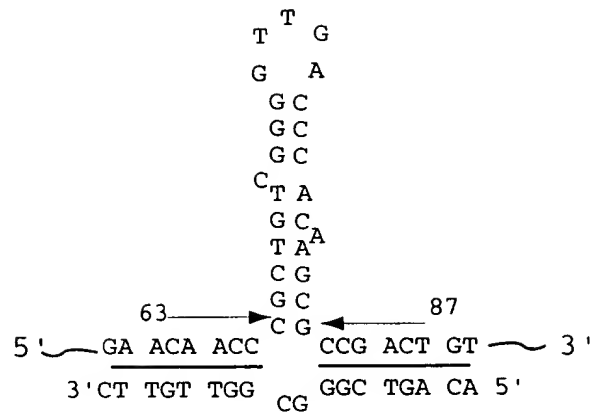
FIGURE 42

FIGURE 44A

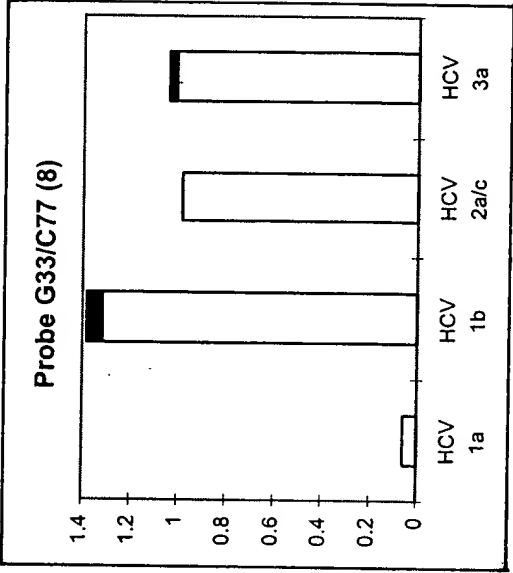
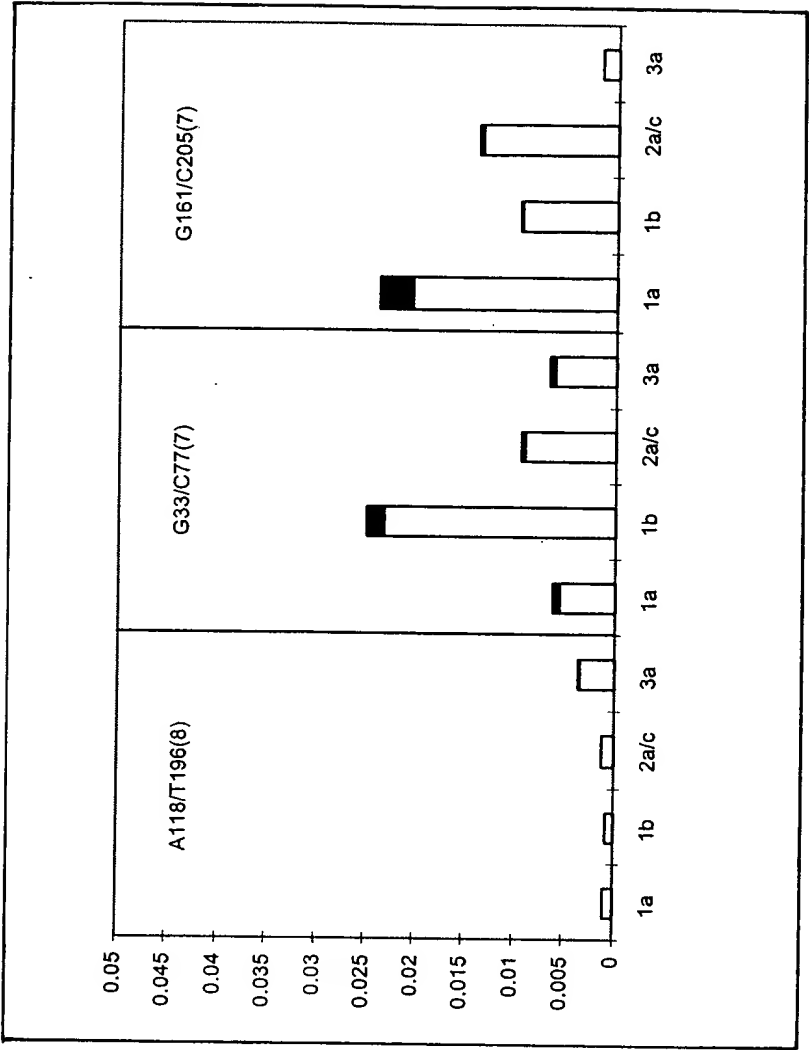


FIGURE 44B



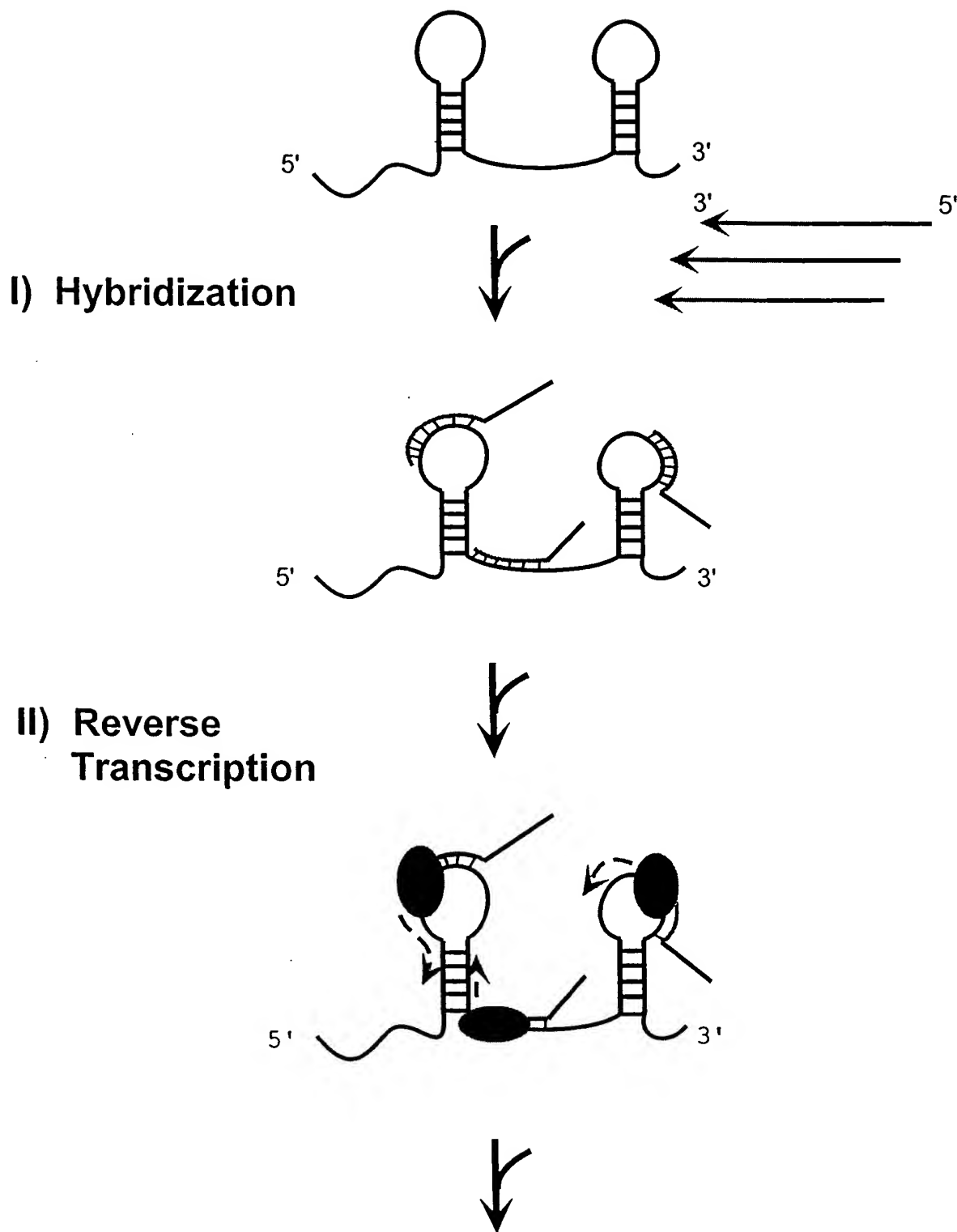
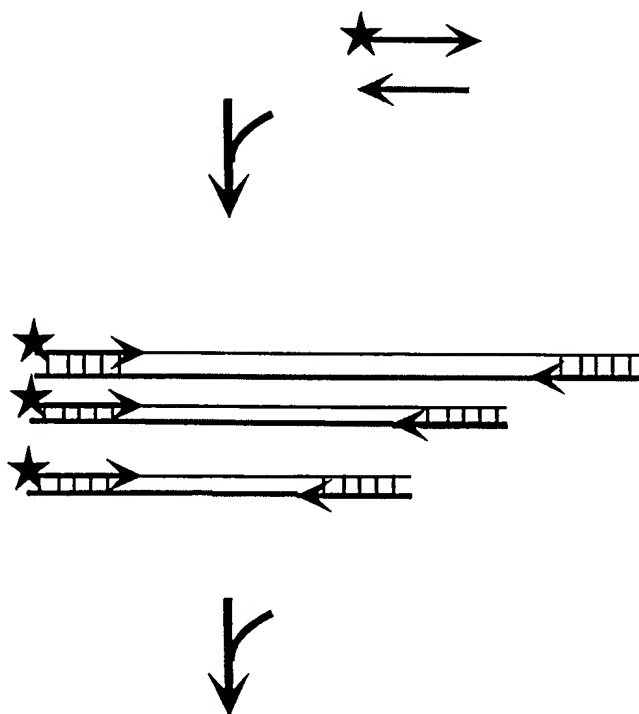


FIGURE 45A

III) PCR



IV) PAGE with Sequencing Ladder

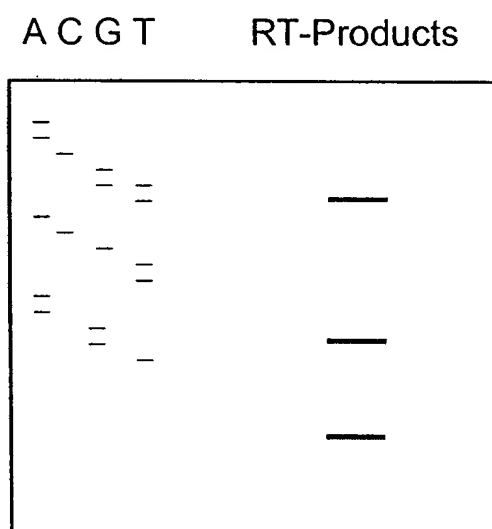
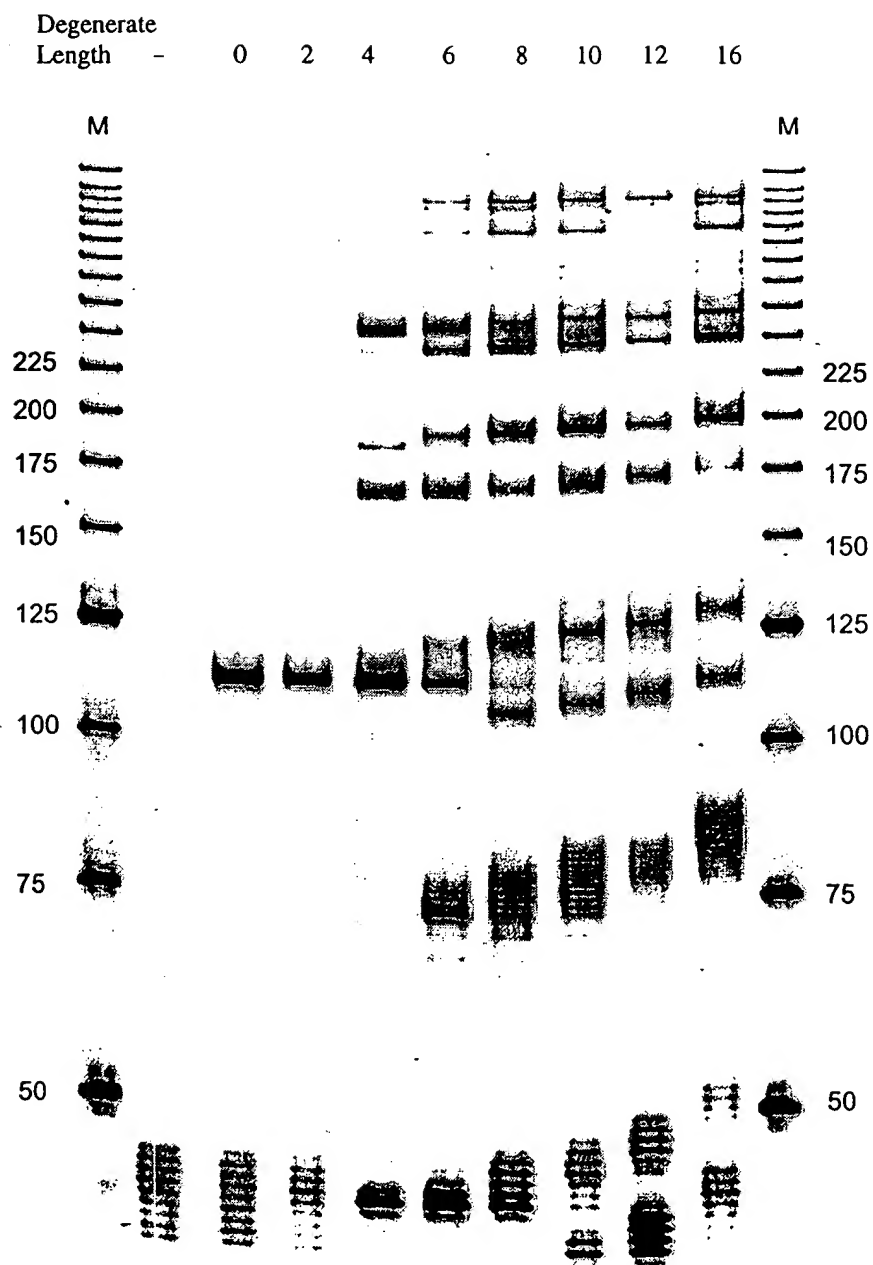


FIGURE 45B

FIGURE 46



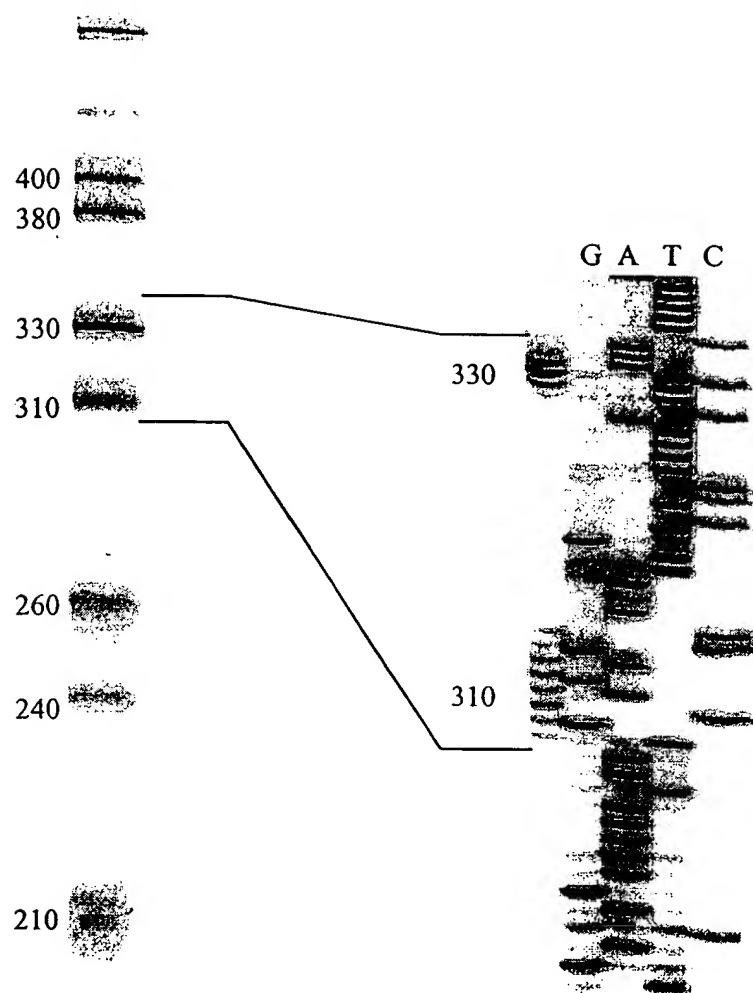


FIGURE 47

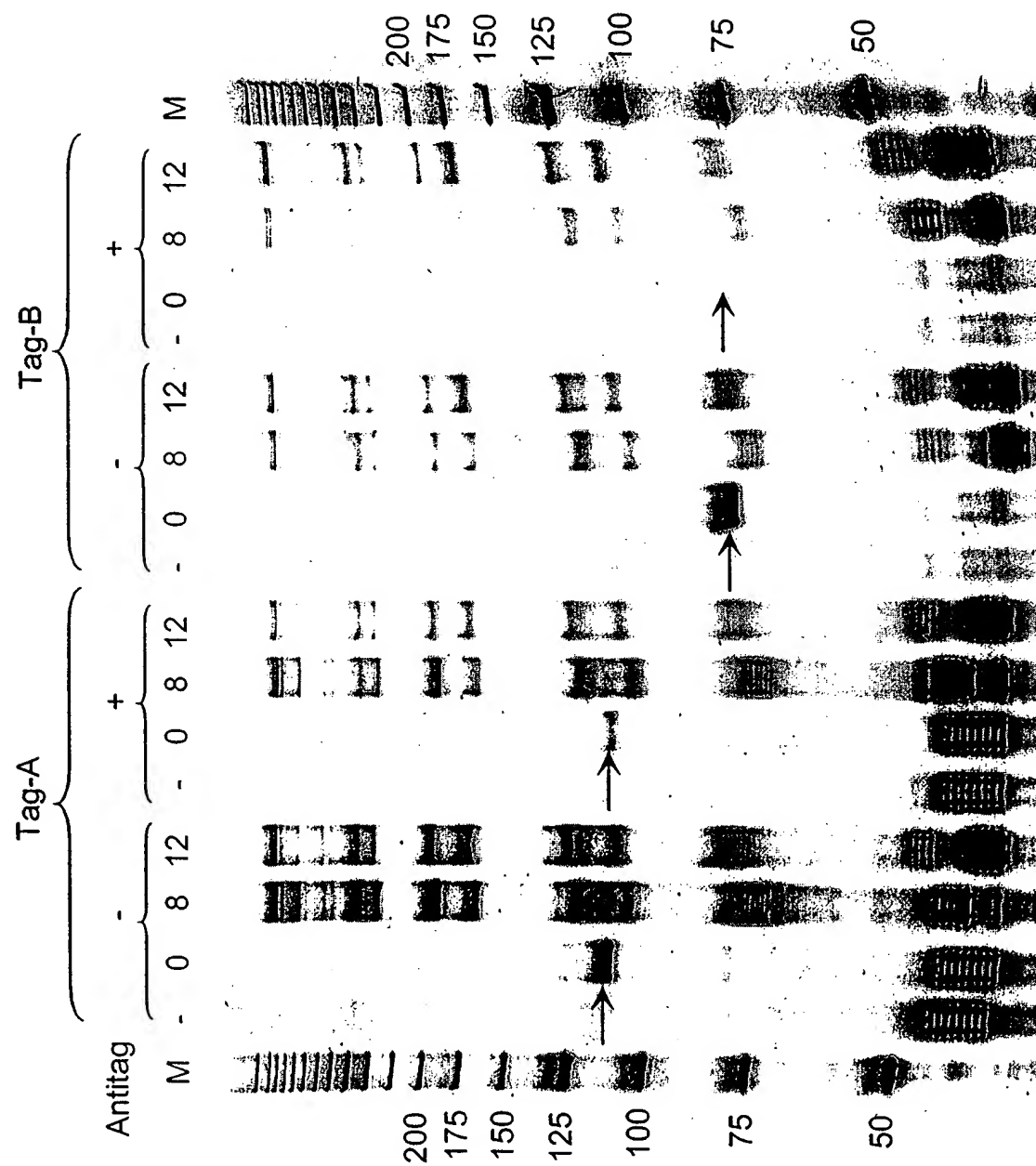


FIGURE 48

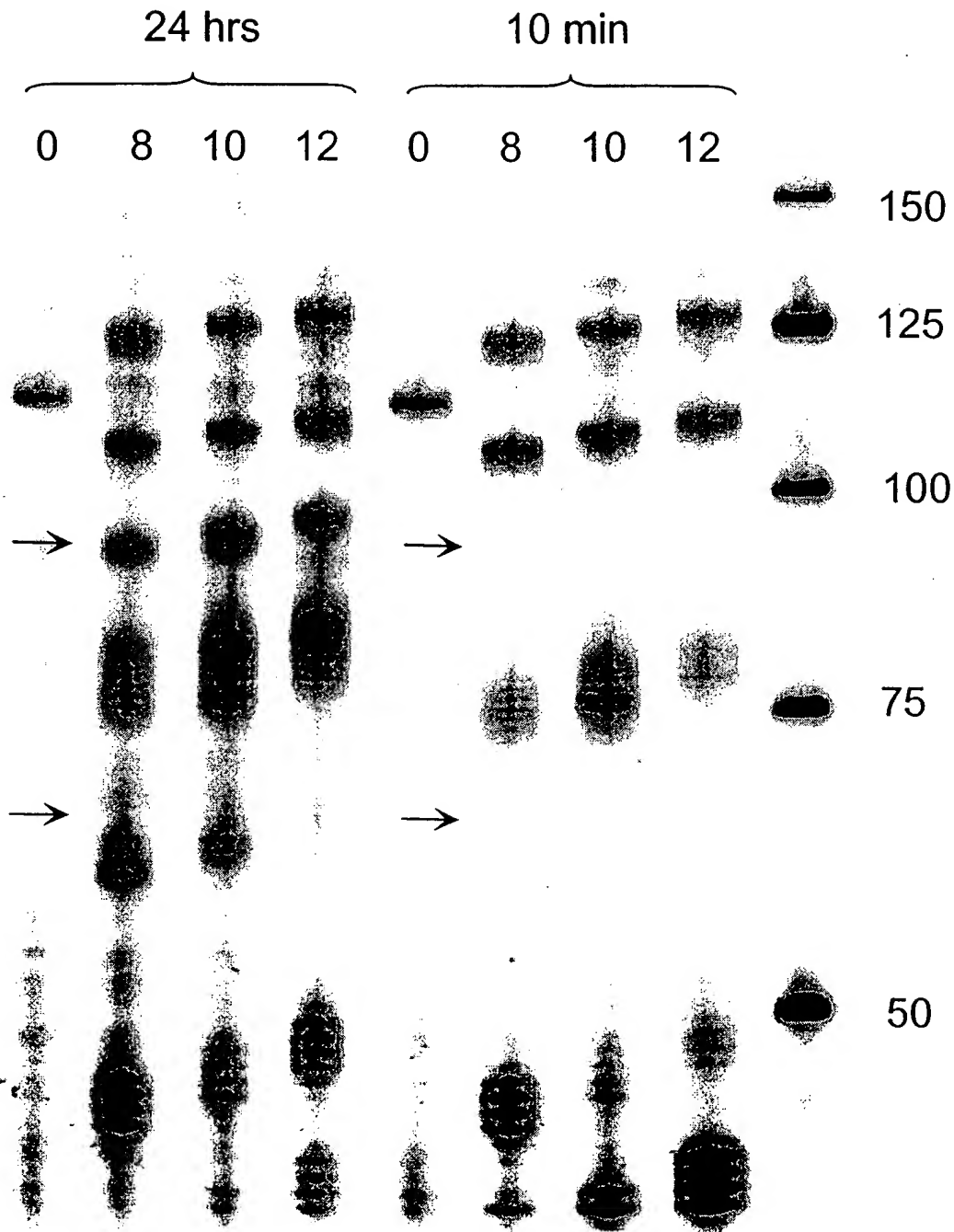


FIGURE 49

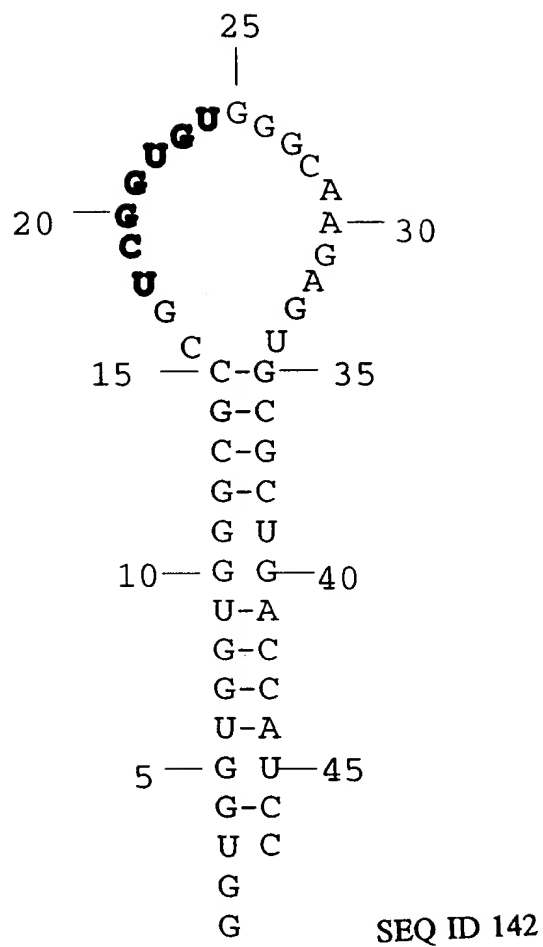


FIGURE 50A

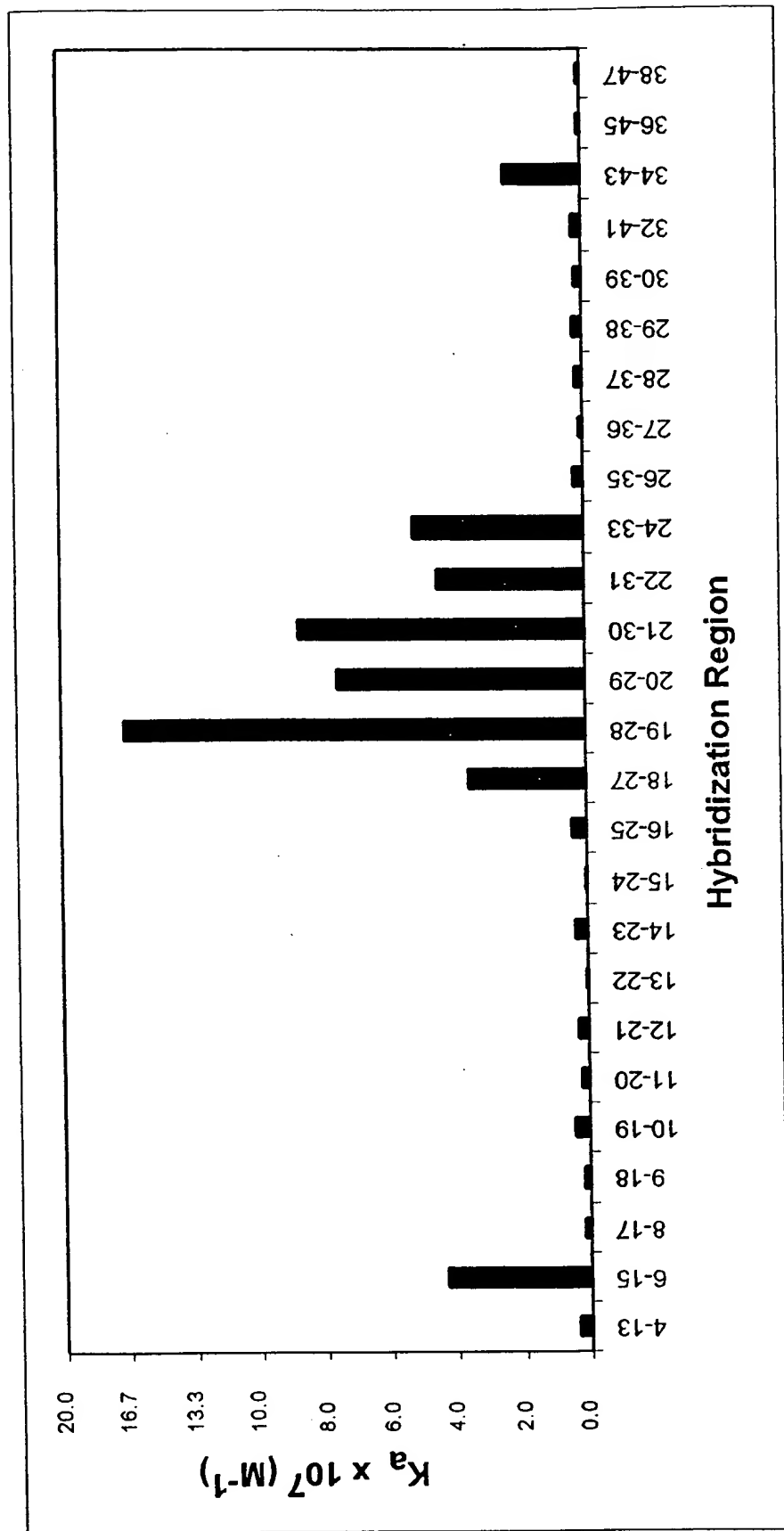


FIGURE 50B

FIGURE 51

1 ACACUUGCUU UUGACACAAC UGUGUUUACU UGC**AAUCCCC** CAAAACAGAC

51 AGA**AUGGUGC** AUCUGUCCAG UGAGGAGA**AAG UCUGCGGUCA** CUGCCCUGUG

101 GGGCAAGGUG AAUGUGGAAG AAGUUGGUGG UGAGGCCUG GGCAGGCUGC

151 UGGUUGUCUA CCCAUGGACC CAGAGGUUCU UCGAGUCCUU UGGGGACCUG

FIGURE 52A

ISIS 1571(-) ISIS 3067(+)
1 GCGCCCC AGT CGACGCTGAG CTCCTCTGCT ACTCAGAGTT

ISIS 1570(+)
41 GCA**ACCTCAG** CCTCGCTATG GCTCCCAGCA GCCCCGGCC
81 CGCGCT**GCCC** GCACTCCTGG TCCTGCTCGG GGCTCTGTTC
121 CCAGGACCTG GCAATGCCCA GACATCTGTG **TCCCCCTCAA**
161 AAGTCATCCT GCCCCGGGGA GGCTCCGTGC TGGTGACATG
201 **CAGCACCTCC** TGTGACC**AGC** CCAAGTTGTT GGGCATAGAG
241 **ACCCCGTTGC** CTAAAAAGGA GTTGCTCCTG CCTGGGAACA
281 ACCGGAAGGT GTATGAACTG AGCAATGTGC AAGAAGATAG

ISIS 1934(-)
321 CCAACCAATG TGCTAT**TCAA** ACTGCCCTGA TGGGCAGTCA
361 ACAGCTAAAA **CCTTCCTCAC** CGT**G**TA**CTGG** ACTCCAGAAC
401 GGGTGGA**ACT** **GGCACCCCTC** CCCTCTTGGC AGCCAGTGGG
441 CAAGAACCTT ACCCTACGCT GCCAGGTGGA GGGTGGGG**CA**
481 **CCCCGGGCCA** ACCTCACCGT GGTGCTGCTC CGTGGGGAGA

FIGURE 52B

521 AGGAGCTGAA ACGGGAGCCA GCTGTGGGGG AGCCCGCTGA
as 610
561 GGTCACGACC ACGGTGCTGG TGAGGAGAGA TCACCATGGA
601 GCCAATTTCT **CGTGCCGCAC** TGA ACTGGAC CTGCGGCCCC
641 AAGGG**CTGGA** GCTGT TTGAG AAC**ACCTCGG** CCCCCTACCA
681 GCTCCAGACC TTTGTCCT**TGC CAGCGACTCC** CCCACA ACTT
721 GTCAGCCCCC GGGTCCTAGA GGTGGACACG CAGGGGACCG
761 TGGTCTGTTC CCT**TGGACGGG** CTGTTCCCAG TCT**CGGAGGC**
801 CCAGGTCCAC CTGGCACTGG GGGACCAGAG GTTGAACCCC
841 ACAGTCACCT ATGGCAACGA CTCCTTCTCG GCCAAGGCCT
881 CAGTCAGTGT GACCGCAGAG GACGAGGGCA CCCAGCGGCT
921 GACGTGTGCA GTAATACTGG GGAACCAGAG **CCAGGAGACA**
961 CTGCAGACAG **TGACCATCTA** CAGCTTTCCG **GCGCCCAACG**
1001 TGATTCTGAC GAAGCCAGAG GTCTCAGAAG GGACCGAGGT

FIGURE 52C

1041 GACAGTGAAG TGT**GAGGCCC** ACCCTAGAGC CAAGGTGACG

1081 CTGAATGGGG TTCCAGCCCA GCCACTGGGC CCGAGGGCCC

1121 AGCTCCTGCT GAAGGCCACC CCAGAGGACA **ACGGGCGCAG**

1161 CTTCTCCTGC TCTGCAACCC TGGAGGTGGC CGGCCAGCTT

as 1220 (+)

1201 **ATACACAAGA** ACCAGACCCG GGAGCTTCGT GTCCTGTATG

1241 **GCCCCCGACT** GGACGAGAGG GATTGTCCGG GAAACTGGAC

1281 GTGGCCAGAA AATT**CCCAGC** **AGACTCCAAT** GTGCCAGGCT

1321 TGGGGGAACC CATTGCCCCG GCTCAAGTGT CTAAAGGATG

ISIS 1547 (+)

1361 GCACTT**TCCC** ACTGCCCATC **GGGGAATCAG** TGA CTGTGCAC

1401 TCGAGATCTT **GAGGGCACCT** ACCTCTGTCTG GGCCAGGAGC

1441 ACTCAAGGGG AGGTCACCCG CGAGGTGACC GTGAATGTGC

1481 TCTCCCCCG GTATGAGATT GTCATCATCA CTGTGGTAGC

1521 AGCCGCAGTC **ATAATGGGCA** CT**GCAGGCCT** **CAGCACGTAC**

FIGURE 52D

1561 CTCTATAACC GCCAGCGGAA GATCAAGAAA TACAGACTAC

as 1630 as 1630h(+++)

1601 AACAGGCCCA AAAAGGGACC CCCATG AAAC CGAACACACA

ISIS 1938 (+)

1641 AGCCACGCCT CCCTGAACCT ATCCCGGGAC AGGGCCTCTT

1681 CCTCGGCCTT CCCATATTGG TGGCAGTGGT GCCACACTGA

1721 ACAGAGTGGA AGACATATGC CATGCAGCTA CACCTACCGG

1761 CCCTGGGACG CCGGAGGACA GGGCATTGTC CTCAGTCAGA

1801 TACAACAGCA TTTGGGGCCA TGGTACCTGC ACACCTAAAA

1841 CACTAGGCCA CGCATCTGAT CTGTAGTCAC ATGACTAAGC

1881 CAAGAGGAAG GAGCAAGACT CAAGACATGA TTGATGGATG

ISIS 1939 (+)

1921 TTAAAGTCTA GCCTGATGAG AGGGGAAGTG GTGGGGGAGA

1961 CATAGCCCCA CCATGAGGAC ATACAACTGG GAAATACTGA

2001 AACTTGCTGC CTATTGGGTA TGCTGAGGCC CACAGACTTA

2041 CAGAAGAAGT GGCCTCCAT AGACATGTGT AGCATCAAAA

FIGURE 52E

ISIS 2302 (+)

2081 CAC**AAAGGCC** CACACTTCCT GACGGATGCC AGCTTGGGCA

2121 CTGCTGTCTA **CTGACCCCAA** CCCTTGATGA TATGTATTTA

ISIS 1572

2161 TTCATTTGTT ATTT**TACCAG** CTATTTATTG AGTGTCTTTT

2201 ATGTAGGCTA AATGAACATA GGTCTCTGGC CTCACGGAGC

2241 TCCCAGTCCA TGTCACATTC AAGGTCACCA GGTACAGTTG

2281 TACAGGTTGT ACACTGCAGG AGAGTGCCTG GCAAAAAGAT

2321 CA**AATGGGGC** TGGGACTTCT CATTGGCCAA CCTGCCTTTC

2361 CCCAGAAGGA GTGATTTTTTC TAT**CGGCACA** AAAGCACTAT

2401 ATGGACTGGT AATGGTTCAC AGGTTCAGAG ATTACCC**AGT**

2441 **GAGGCCTTAT** TCCTCC**CTTC** CCCCCAAAAC TGACACCTTT

2481 GT**TAGCCACC** **TCCCCACCCA** CATACATTTT TGCCAGTGTT

2521 CACAATGACA CTCAGCGGTC ATGTCTGGAC ATGAGTGCCC

2561 AGGGA**ATATG** **CCCAAGCTAT** GCCTTGTCTT CTTGTCCTGT

FIGURE 52F

2601 TTGCATTTCA CTGGGAGCTT GCACTATTGC AGCTCCAGTT

2641 TCCTGCAGTG ATCAGGGTCC TGCAAGCAGT GGGGAAGGGG

2681 GCCAAGGTAT TGGAGGACTC CCTCCCAGCT TTGGAAGGGT

2721 CATCCGCGTG TGTGTGTGTG TGTATGTGTA GACAAGCTCT

2761 CGCTCTGTCA CCCAGGCTGG AGTGCAGTGG TGCAATCATG

2801 GTTCACTGCA GTCTTGACCT TTTGGGCTCA AGTGATCCTC

2841 CCACCTCAGC CTCCTGAGTA GCTGGGACCA TAGGCTCACA

2881 ACACCACACC T

FIGURE 53A

1 CACAUUGUUC UGAUCAUCUG AAGAU CAGCU AUUAGAAGAG
site 80
 41 AAAGAU CAGU UAAGUCCUUU GGACCUGAUC AGCUUGAUAC
site 120
 81 AAGAACUACU GAUUUCAACU UCUUUGGCUU AAUUCUCUCG
 121 GAAACGAUGA AAUAUACAAG UUAUAUCUUG GCUUUUCAGC
 161 UCUGCAUCGU UUUGGGUUCU CUUGGCUGUU ACUGCCAGGA
site 210
 201 CCCAUAUGUA **CAAGAAGCAG** AAAACCUUAA GAAAUUUUU
site 240 site 260
 241 AAUGCAGGUC AUUCAGAUGU AGCGGAUAAU GGAACUCUUU
 281 UCUUAGGCAU UUUGAAGAAU UGGAAAGAGG AGAGUGACAG
site 330
 321 AAAAUAAUG **CAGAGCCAAA** UUGUCUCCUU UUACUUCAAA
site 380 site 400
 361 CUUUUUAAAA ACUUUAAAGA UGACCAGAGC AUCCAAAAGA
 401 GUGUGGAGAC CAUCAAGGAA GACAUGAAUG UCAAGUUUUU
 441 CAAUAGCAAC AAAAAGAAAC GAGAUGACUU CGAAAAGCUG

FIGURE 53B

481 ACUAAUUAUU CGGUAACUGA CUUGAAUGUC CAACGCAAAG
 521 CAAUACAUGA ACUCAUCCAA GUGAUGGCUG AACUGUCGCC site 560
 561 AGCAGCUAAA ACAGGGAAGC GAAAAAGGAG UCAGAUGCUG site 570
 601 UUUCGAGGUC GAAGAGCAUC CCAGUAAUGG UUGUCCUGCC
 641 UACAAUAUUU GAAUUUUAAA UCUAAAUCUA UUUAUUAAUA
 681 UUUAACAUA UUUAUAUGGG GAAUAUAUUU UUAGACUCAU
 721 CAAUCAAAUA AGUAUUUAUA AUAGCAACUU UUGUGUAAUG
 761 AAAAUGAAUA UCUAUUAAUA UAUGUAUUUAU UUAUAAUUC
 801 UAUAUCCUGU GACUGUCUCA CUUAAUCCUU UGUUUUCUGA
 841 CUAUUUAGGC AAGGCUAUGU GAUUACAAGG CUUUAUCUCA site 850 site 860 site 880
 881 GGGGCCAACU AGGCAGCCAA CCUAAGCAAG AUCCCAUGGG site 890 site 910
 921 UUGUGUGUUU AUUUCACUUG AUGAUACAAU GAACACUUUAU
 961 AAGUGAAGUG AUACUAUCCA GUUACUA

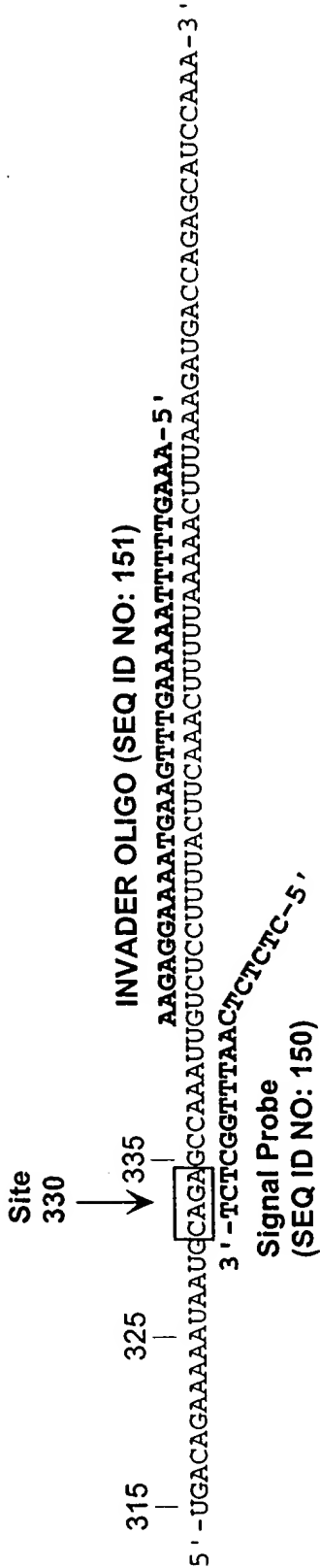


FIGURE 54A

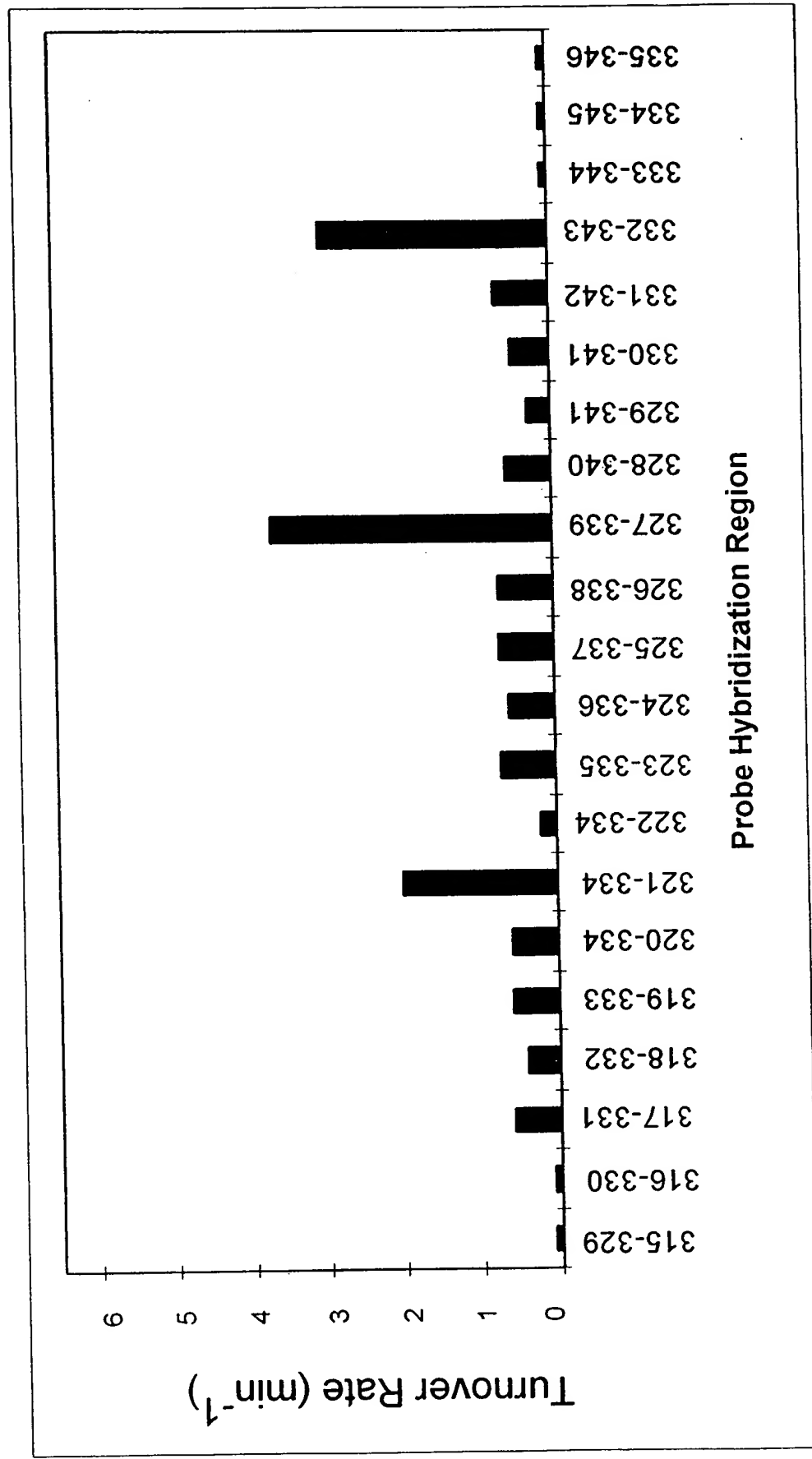


FIGURE 54B

FIGURE 55A

SEQ ID NO:158

Primer 1

460 GGUCUCUCUG GUUAGACCAG AUCUGAGCCU GGGAGCUCUC UGGCUAACUA

510 GGGAACCCAC UGCUUAAGCC UCAAUAAAGC UUGCCUUGAG UGCUUCAAGU

560 AGUGUGUGCC CGUCUGUUGU GUGACUCUGG UAACUAGAGA UCCCUCAGAC

Primer 2

610 CCUUUUAGUC AGUGUGGAAA AUCUCUAGCA GUGGCGCCCG AACAGGGACC

660 UGAAAGCGAA AGGGAAACCA GAGGAGCUCU CUCGACGCAG GACUCGGCUU

710 GCUGAAGCGC GCACGGCAAG AGGCGAGGGG CGGCGACUGG UGAGUACGCC

760 AAAAUUUUG ACUAGCGGAG GCUAGAAGGA GAGAGAUGGG UGCGAGAGCG

Primer 3

810 UCAGUAUUAA GCGGGGGAGA AUUAGAUCGA UGGGAAAAAA UUCGGUUAAG

860 GCCAGGGGGA AAGAAAAAAU AUAAAUUAAA ACAUAUAGUA UGGGCAAGCA

910 GGGAGCUAGA ACGAUUCGCA GUUAAUCCUG GCCUGUUAGA AACAUAGAA

960 GGCUGUAGAC AAUACUGGG ACAGCUACAA CCAUCCCUUC AGACAGGAUC

Primer 4

1010 AGAAGAACUU AGAUCAUUAU AUAAUACAGU AGCAACCCUC UAUUGUGUGC1060 AUCAAAGGAU AGAGAUAAAA GACAC**CAAGG** AAGCUUUAGA CAAGAUAG**AG**

FIGURE 55B

1110 **GAAGAGCAAA** ACAAAGUAA GAAAAAGCA CAGCAAGCAG CAGCUGACAC

1160 **AGGACACAGC** AAUCAGGUCA GCCAAAAUUA CCCUAUAGUG CAGAACAUC

Primer 5

1210 **AGGGGCAAAU** GGUACAUCAG GCCAUAUCAC CUAGAACUUU AAAUGCAUGG

1260 GUAAAAGUAG UAGAAGAGAA GGCUUUCAGC CCAGAAGUGA UACCCAUGUU

1310 UUCAGCAUUA UCAGA**AGGAG** **CCACCCCACA** AGAUUUAAAC ACCAUGCUAA

1360 ACACAGUGGG GGGACAUC**AA** **GCAGCCAUGC** AAAUGUUAAA AGAGACCAUC

Primer 6

1410 **AAUGAGGAAG** CUGCAGAAUG GGAUAGAGUG CAUCCAGUGC AUGCAGGGCC

1460 UAUUGC**ACCA** GGCCAGAUGA GAGA**ACCAAG** **GGGAAGUGAC** AUAGCAGGAA

1510 CUACUAGUAC CCUUCAGGAA CAAAUAGGAU GGAUGACAAA UAAUCCACCU

1560 AUCCCAGUAG GAGAAAUUUA UAAAGAUGG AUAUCCUGG GAUUAUUAA

Primer 7

1610 AAUAGUAAGA AUGUAUAGCC CUACCAGCAU UCUGGACAU AGACAAGGAC

1660 CAAAGGAACC CUUUAGAGAC UAUGUAGACC GGUUCUAUAA AACUCUAAGA

1710 **GCCGAGCAAG** CUUC**ACAGGA** GGUAAAAAU **UGGAUGACAG** AAACCUUGUU

FIGURE 55C

1760 GGUCCAAAAU GCGAACCCAG AUUGUAAGAC UAUUUUAAAA GCAUUGGGAC

Primer 8

1810 **CAGCGGCUAC** ACUAGAAGAA AUGAUGACAG CAUGUCAGGG AGUAGGAGGA

1860 CCCGGCCAUU AGGCAAGAGU UUUGGCUGAA GCAAUGAGCC AAGUAACAAA

1910 UUCAGCUACC AUAAUGAUGC **AGAGAGGCAA** UUUUAGGAAC CAAAGAAAGA

1960 UUGUUAAGUG UUUCAAUUGU GGCAAAGA**AG** **GGCACACAGC** CAGAAAUUGC

2010 AGGGCCCCUA GGAAAAAGGG CUGUUGGAAA UGUGGAAAGG AAGGACACCA

2060 AAUGAAAGAU UGUACUGAGA G

FIGURE 56

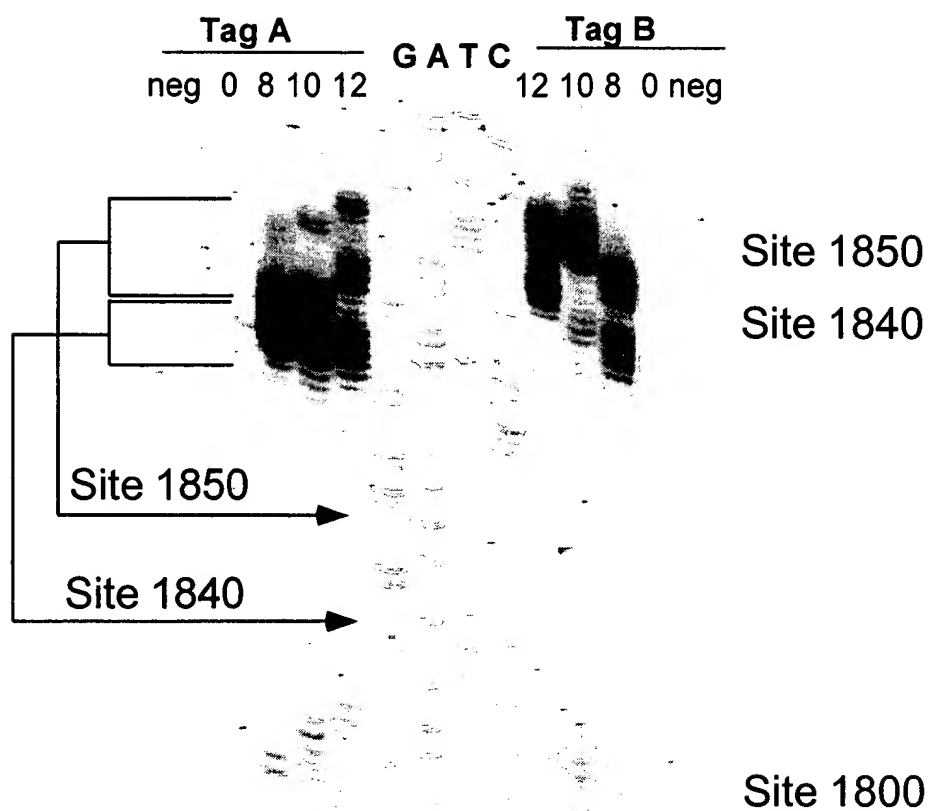


FIGURE 57

(SEQ ID NO:188)	CGTATTCGGTCTCAAAACCGACTTGCT-5'	13
(SEQ ID NO:187)	AGGTATTCGGTCTCAAAACCGACT	12
(SEQ ID NO:186)	ACGGTATTCGGTCTCAAAACCGAC	10=11
(SEQ ID NO:185)	CCCGGTATTCGGTCTCAAAACCGA	9
(SEQ ID NO:184)	CGCCGGTATTCGGTCTCAAAACCG	8
(SEQ ID NO:183)	CGCCGGTATTCGGTCTCAAAACCG	7
(SEQ ID NO:182)	AGGCCGGTATTCGGTCTCAAAAC	6
(SEQ ID NO:181)	ATGGCCGGTATTCGGTCTCAAAA	5
(SEQ ID NO:180)	ACTGGCCGGTATTCGGTCTCAAA	4
(SEQ ID NO:179)	ACCTGGCCGGTATTCGGTCTCAA	3
(SEQ ID NO:178)	ATCCTGGCCGGTATTCGGTCTCA	2
(SEQ ID NO:177)	ACTCCTGGCCGGTATTCGGTCTC	1
5'-CAUGCAGGAGUAGGAGGCCCGCCCAUAAAGCAAGUUUGGCUGAAAGCAAUGAG-3'	(SEQ ID NO:158)	
1 CAGTCCCTCATC	(SEQ ID NO:164)	
2 AGTCCCTCATCC	(SEQ ID NO:165)	
3 GTCCCTCATCCT	(SEQ ID NO:166)	
4 TCCCTCATCCTC	(SEQ ID NO:167)	
5 CCTCATCCTCC	(SEQ ID NO:168)	
6 CCTCATCCTCCT	(SEQ ID NO:169)	
7 CTCATCCTCCTG	(SEQ ID NO:170)	
8 TCATCCTCCTGG	(SEQ ID NO:171)	
9 CATCCTCCTGGG	(SEQ ID NO:172)	
10 ATCCTCCTGGGC	(SEQ ID NO:173)	
11 TCCTCCTGGGC	(SEQ ID NO:174)	
12 CCTCCTGGGCC	(SEQ ID NO:175)	
13 CTCCTGGGCCGAAA-FL-5'	(SEQ ID NO:176)	

FIGURE 58

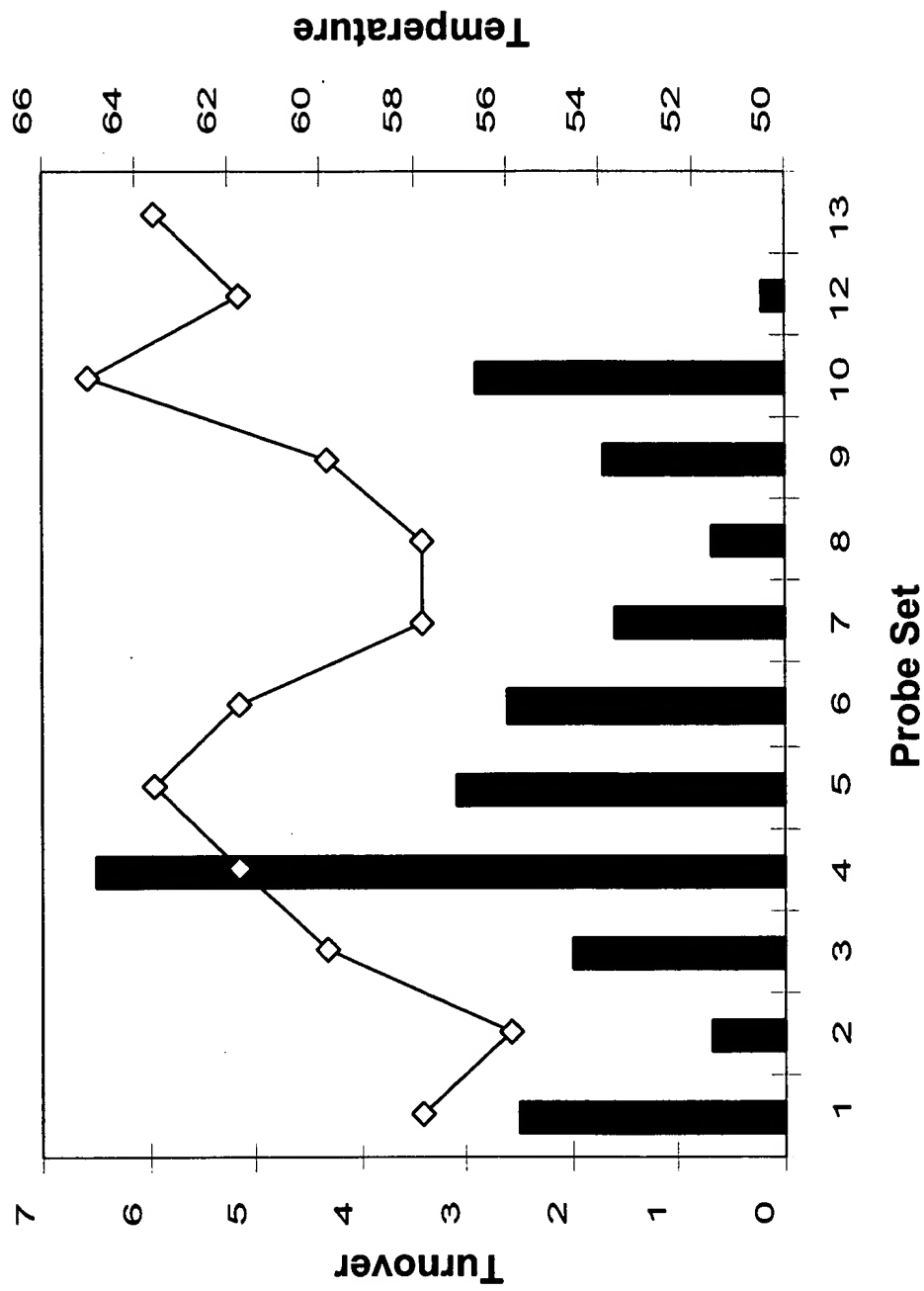


FIGURE 59

(SEQ ID NO:180)
ACTGGGCCGGTATTCCGTTCTCAA
5' -CAUGUCAGGCAGUAGGAGGACCCGGCCAUAAGGCAAGAGUUUUGGCUGAAGCAAUGAG-3'
(SEQ ID NO:158)
TCCCTCATCCTCCTCCGCACTGCC-5',
(SEQ ID NO:189)

5' -AGGGAGTAGGAGGAGG-3'
(SEQ ID NO:190)

(SEQ ID NO:191) (F) (Q) (SEQ ID NO:193)
5' - CCGTCACGCCTCC CAAC GCTTCCCTCCG-3'
3' -TGGCAGTCCGGAGGTTGACGAAGAAGGC-5'
(SEQ ID NO:192)

FIGURE 60

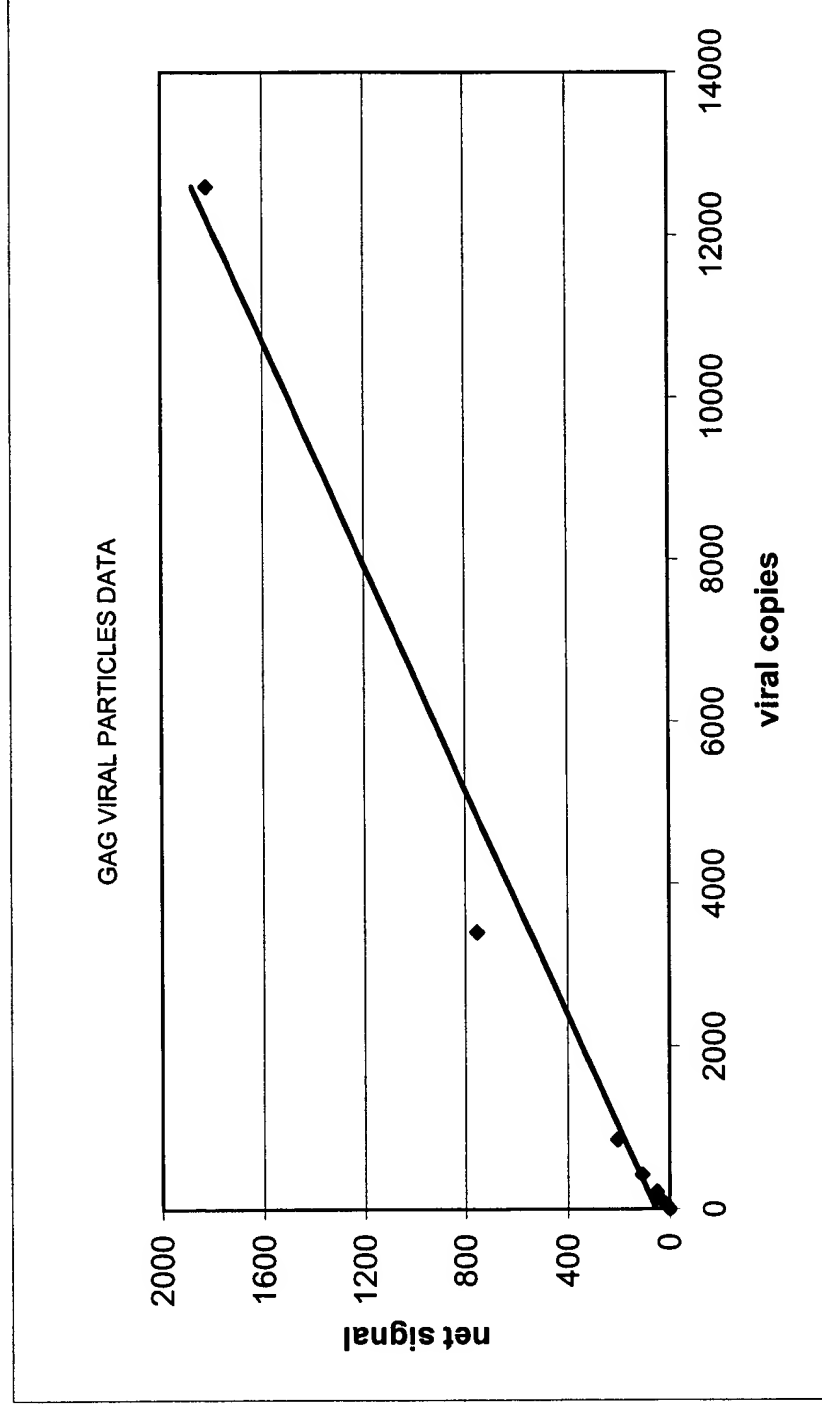


FIGURE 61A

SEQ ID NO:159

primer 1
3300 AGCUGGACUG UCAAUGACAU ACAGAA**GUUA** **GUGGGG**AAAU UG**AAUUGGGC**

3350 AAGUCAGAUU **UACCCAGGGA** UUA**AAGUAAG** GCAAUUAUGU AAACUCCUUA

3400 GAGGAACCAA AGCACUAACA GAAGUAAUAC CACUAACAGA AGAAGCAGAG

3450 CUAGAA**CUGG** CAGAAAACAG AGAGAUUCUA AAAGAACCAG UACAUGGAGU

primer 2
3500 GUAUUAUGAC CCAUCAAAAG ACUUAUAGC AGAAAU**ACAG** **AAGCAGGGGC**

3550 **AAGGCCAAUG** GACAUAUCAA AUUUAU**CAAG** AGCCAUUUAA AAAUCUGAAA

3600 ACAGGAAAAU AUGCAAGAAU **GAGGGGUGCC** CACACUAAUG AUGUAAAACA

3650 AUUAACAG**AG** **GCAGUG**CAAA AAUAACCAC AGAAAGCAUA GUAAUAUGGG

primer 3
3700 GAAAGACUCC UAAAUUUAAA CUGCCCAUAC AAAAGGAAAC AUGGGAAACA

3750 UGGUGGACAG AGUAUUGGCA AGCCACCUGG AUUCCUGAGU GGGAGUUUGU

3800 UAAUACCCCU CCCUAGUGA AAUUA**UGGUA** CCAGUUAGAG AAAGAACCCA

3850 UAGU**AGGAGC** AGAAACCUUC UAUGUAGAUG **GGGCAGCUAA** **CAGGGAGACU**

primer 4
3900 AAAUUAGGAA AAGCAGGAUA UGUUACUAAU **AGAGGAAGAC** AAAAAGUUGU

FIGURE 61B

3950 CACCCUAACU GACACAACAA AUCAGAAGAC UGAGUUACAA GCAAUUUAUC
4000 UAGCUUUGCA GGAUUC**CGGA** UUAGAAGUAA ACAUAGUAAAC AGACUCACAA
4050 UAUGCAUUAG GAAUCAUUA **AGCACAACCA** GAUCAAAGUG AAUCAGAGUU
primer 5
4100 AGUCAAUCAA AUAUAG**GAGC** AGUUAUAAA AAAGGAAAAG GUCUAUC**UGG**
4150 **CAUGGGUACC** AGCACACAAA GGA**AUUGGAG** GAAAUGAACA AGUAGAUAAA
4200 UUAGUCAGUG CUGGAAUCAG GAAAGUACUA UUUUUAGAUG GAAUAGAU**AA**
4250 **GGCCCAAGAU** GAACAUGAGA AAUAUCACAG UAAUUG**GGAGA** GCAAUGGCUA
primer 6
4300 GUGAUUUUAA CCUGCCACCU GUAGUAGCAA AAGAAUAGU **AGCCAGCUGU**
4350 GAUAAAUGUC AGCUAAAAGG AGAAGCCAUG CAUGGACAAG UAGACUGUAG
4400 UCCAGGAUA UGGCAACUAG AUUGUACACA UUUAGAAGGA AAAGUUAUCC
4450 UGGUAGCAGU UCAUGUAGCC AGUGGAUUA UAG**AA**GCAGA AGUUAUUCCA
primer 7
4500 GC**AGAA**CAG **GGCAG**GAAAC AGCAUAUUUU CUUUUAAAAU **UAGCAGGAAG**
4550 **AUGGCCAGUA** AAAACAAUAC AUACUG**ACAA** **UGGCAGCAAU** UUC**ACCGGUG**
4600 CUACGGUUAG GGCCGCCUGU UGGUGGGCGG GAAUCA**AGCA** **GGAAUUUGGA**

FIGURE 61C

4650 AUUCCCUACA AUCCCCAAG UCA**AAGG**AGUA GUAGAAUCUA UGAAUAAAGA

primer 8

4700 AUUAAAGAAA AUUAUAG**GAC** **AGG**UAAGAGA **UCAGGC**UGAA CAUCUUAAGA

4750 CAGCAGUACA AAUGGCAGUA UUCAUCCACA AUUUUAAAAG AAA**AGGGGGG**

4800 AUUGGGGGGU AC**AGUGCAGG** **GGAA**AGAAUA GUAGACAUAA UAGCAACAGA

4850 CAUACAAACU AAAGAAUUAC AAAAACAAAU UACAAAAAUU CAAA AUUUUC

primer 9

4900 GGGUUUAUUA CAG**GGAC**AGC AGAAAUCCAC UUUGGA**AAGG** ACCAGCAAAG

4950 CUCCUCUGGA AAGGUG**AAGG** GGCAGUAGUA AUACAAGUA AUAGUGACAU

5000 AAAA**GUAGUG** CCAAGAAGAA AAGCAAAGAU CAUUAGGGAU UAUGGAAAAC

5050 AGAUGGCAGG UGAUGAUUGU G

FIGURE 62

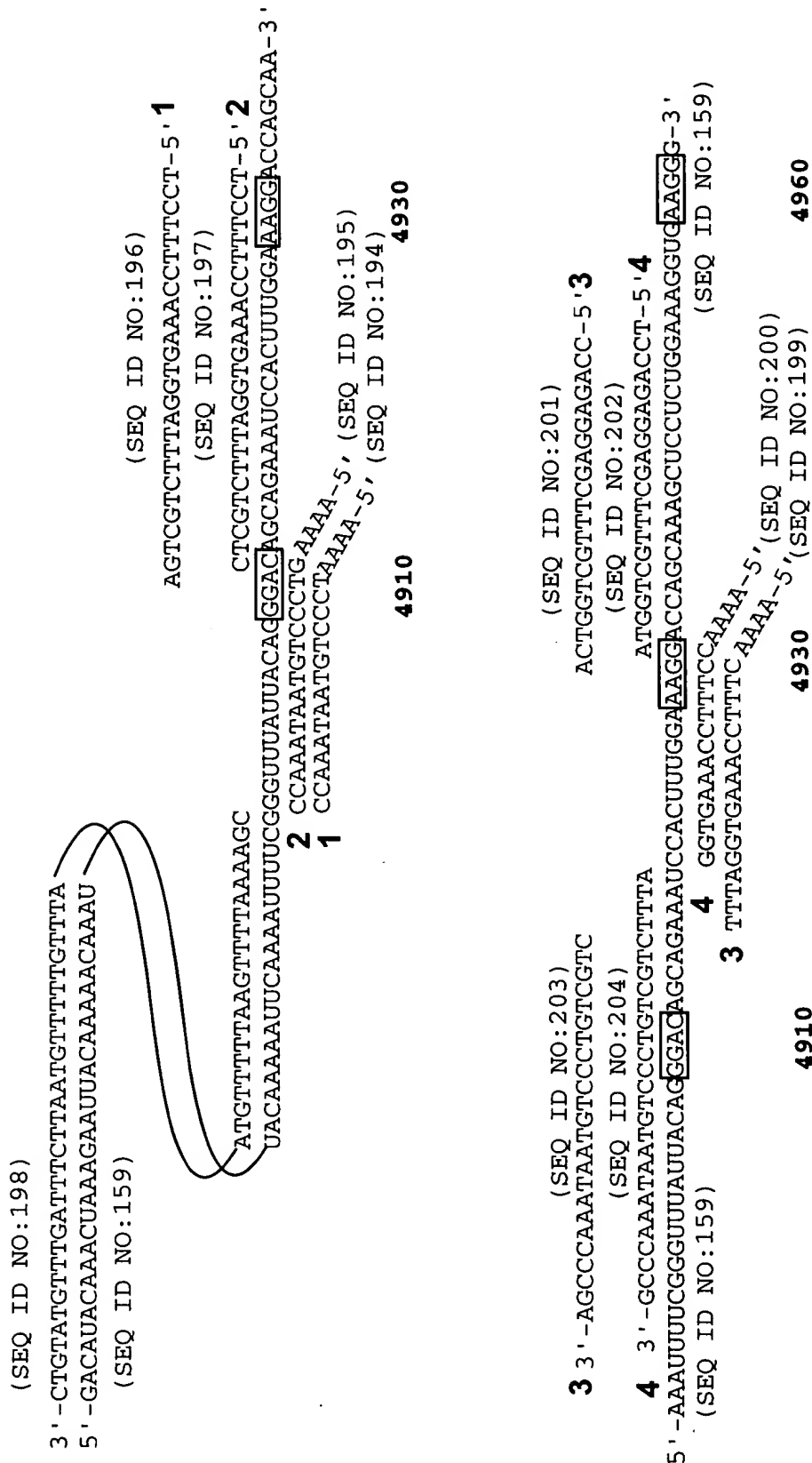


FIGURE 63

(SEQ ID NO:213)
5 3'-TCCTGGTCGTTTCGAGGAGA (SEQ ID NO:209)
ACCCGTCATCATTTATGTTCTATTATCACTGTATTTT-5' **5**
(SEQ ID NO:214)
6 3'-CCTGGTCGTTTCGAGGAGAC (SEQ ID NO:210)
ACCGTCATCATTTATGTTCTATTATCACTGTATTTTC-5' **6**
5'-GTAAGGACCAGCAAGCUCUCUGGAAAGGUAAGGEGCAGUAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUGC-3'
(SEQ ID NO:159) **5000**
4930 6 CTTTCCACTTCCAAA-5'
5 CCTTTCCACTTCAAAA-5', (SEQ ID NO:206)
4960 (SEQ ID NO:205)

(SEQ ID NO:215)
7 3'-TCGAGGAGACCTTTCCAC (SEQ ID NO:211)
CTCATTTATGTTCTATTATCACTGTATTTTTCATCACGG-5' **7**
(SEQ ID NO:216)
8 3'-TCGAGGAGACCTTTCCACT (SEQ ID NO:212)
ACATTATGTTCTATTATCACTGTATTTTTCATCACGG-5' **8**
5'-GTAAGGACCAGCAAGCUCUCUGGAAAGGUAAGGEGCAGUAGUAAUACAAGAUAAUAGUGACAUAAAAGUAGUGCCAAGAA-3'
(SEQ ID NO:159) **5000**
4930 8 TCCCCGTCATAAAA-5', (SEQ ID NO:208)
7 TTCCCCGTCATAAAA-5', (SEQ ID NO:207)
4960

FIGURE 64

1	4790	4810	<p>(SEQ ID NO:224)</p> <p>3'-TCCCCCTAACCCCCCATG 5'-AAGAAAGGGGGGGAAGUGCAGGGGAAGAGAAUAGUAGACAUAAUAGCAACAGACAUACAAACU-3' TCACGTCCCCAAAA-5',(SEQ ID NO:217)</p> <p>(SEQ ID NO:221)</p> <p>ATTTCTTATCATCTGTATTATCGTTGTCTGTATGT-5'</p> <p>(SEQ ID NO:159)</p>
2, 4	4790	4810	<p>(SEQ ID NO:225)</p> <p>3'-CTGTCGTCATGTTTACCGTCATAAGTAGGT 5'-AGACAGCAGUACAAAUAGGCAGUAUUAUCCACAAUUUUUAAAGAAAGGGGGGAUUGGGGGUACAGUGCAGGGGAAG-3' GTTAAATTTTCTTTTCCCATAATA-5',(SEQ ID NO:159)</p> <p>ACCCTAACCCCCCATGTCAC-5'</p> <p>GTAAAAATTTTCTTTTCCCATAATA-5',(SEQ ID NO:220)</p> <p>GTAAAAATTTTCTTTTCCCATAATA-5',(SEQ ID NO:218)</p>
3	4790	4810	<p>(SEQ ID NO:222)</p> <p>ACCCCTAACCCCCCATGTCAC-5' 5'-AAAGGGGGGAUUGGGGGUACAGUGCAGGGGAAGAGAAUAGUAGACAUAAUAGCAACAGACAUACAAACUAAAGAA-3' GTCCCCCTTTCTTAAAA-5',(SEQ ID NO:159)</p> <p>(SEQ ID NO:223)</p> <p>CATCATCTGTATTATCGTTGTCTGTATGTTGATTTC</p> <p>(SEQ ID NO:219)</p>

FIGURE 65

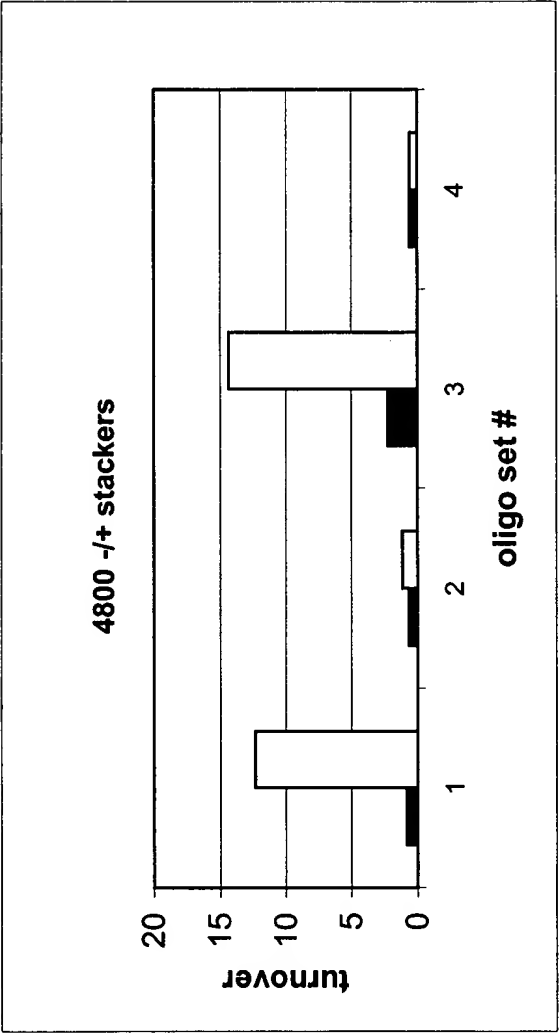


FIGURE 66

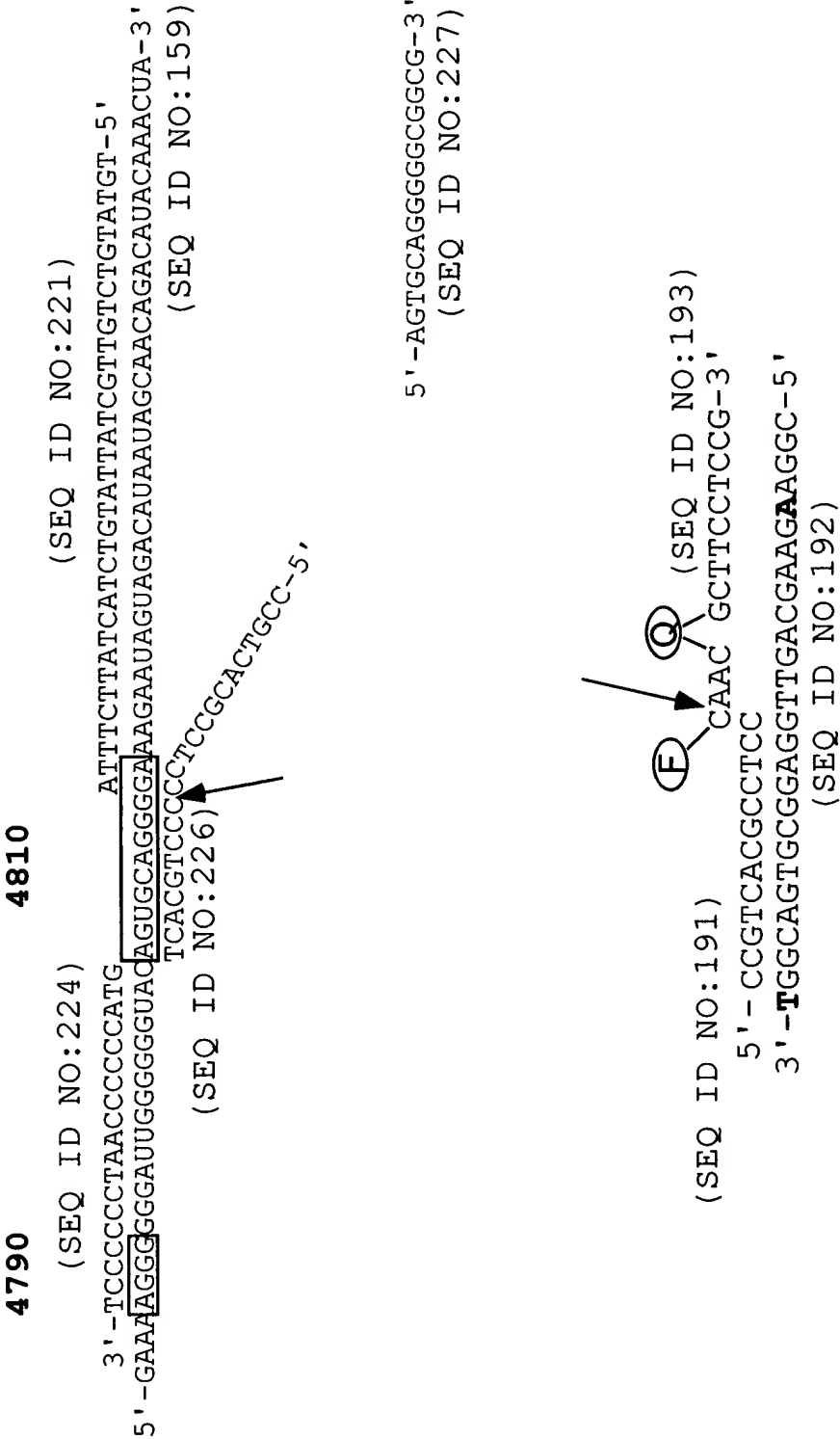


FIGURE 67

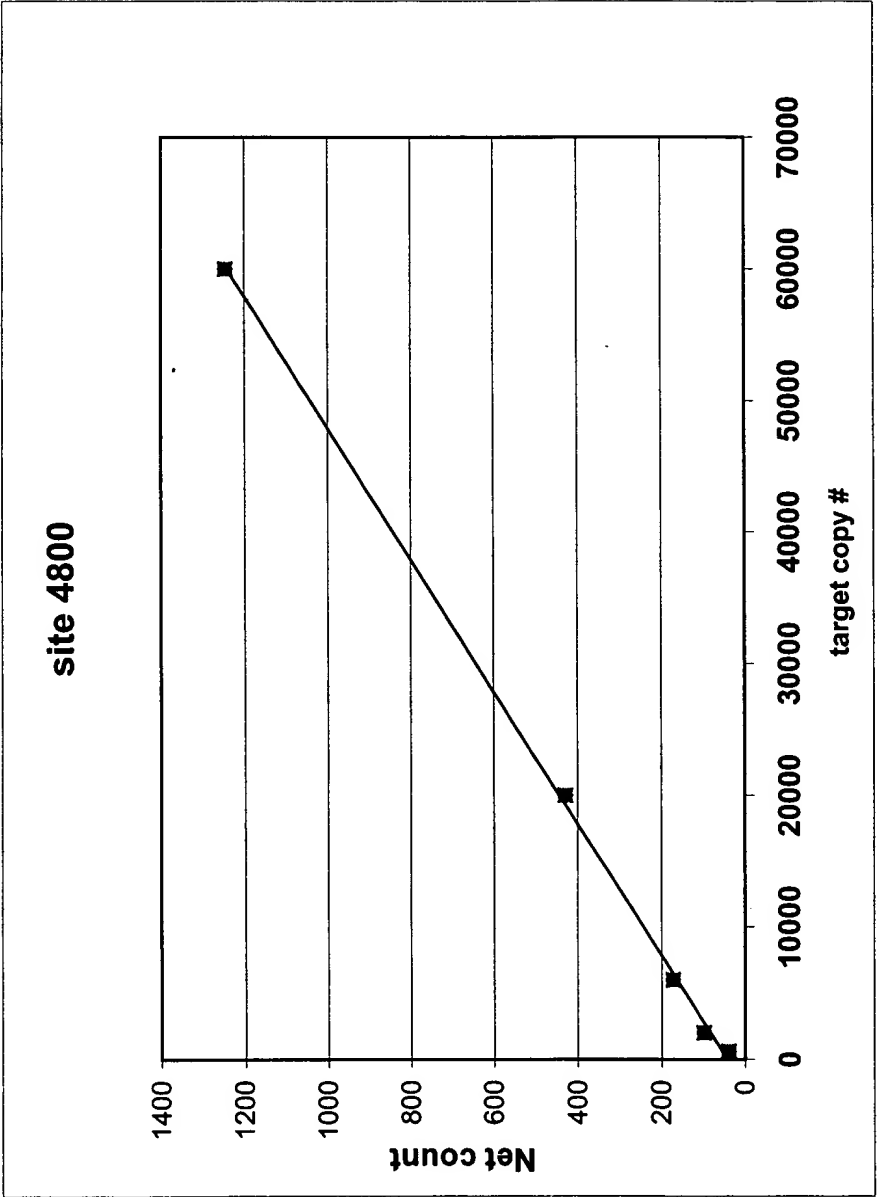


FIGURE 68

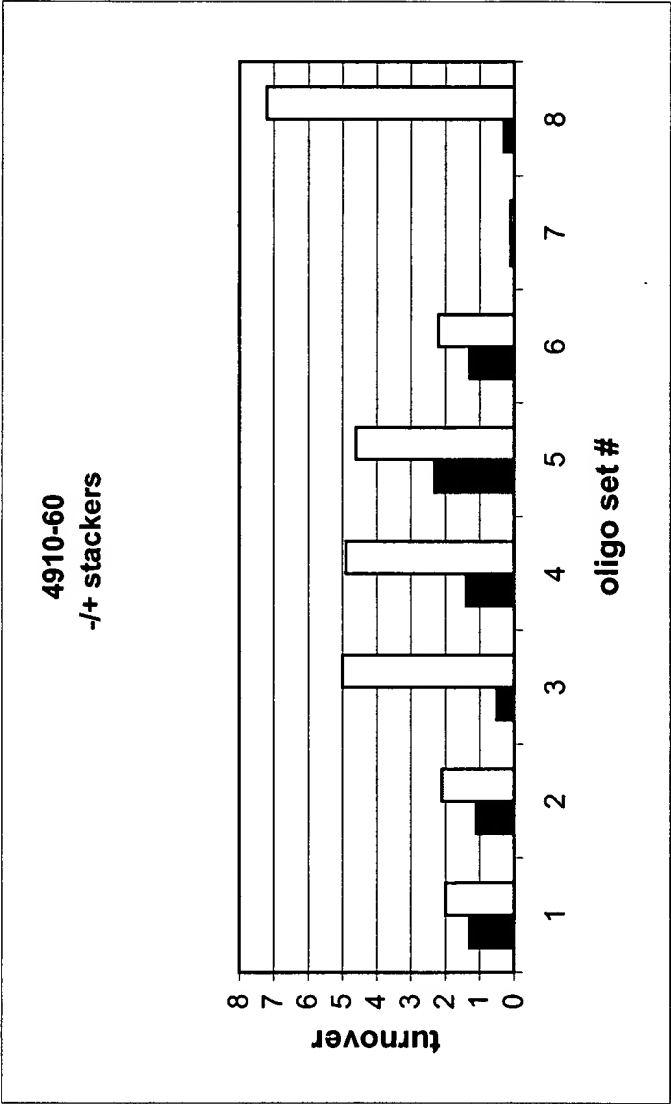


FIGURE 69

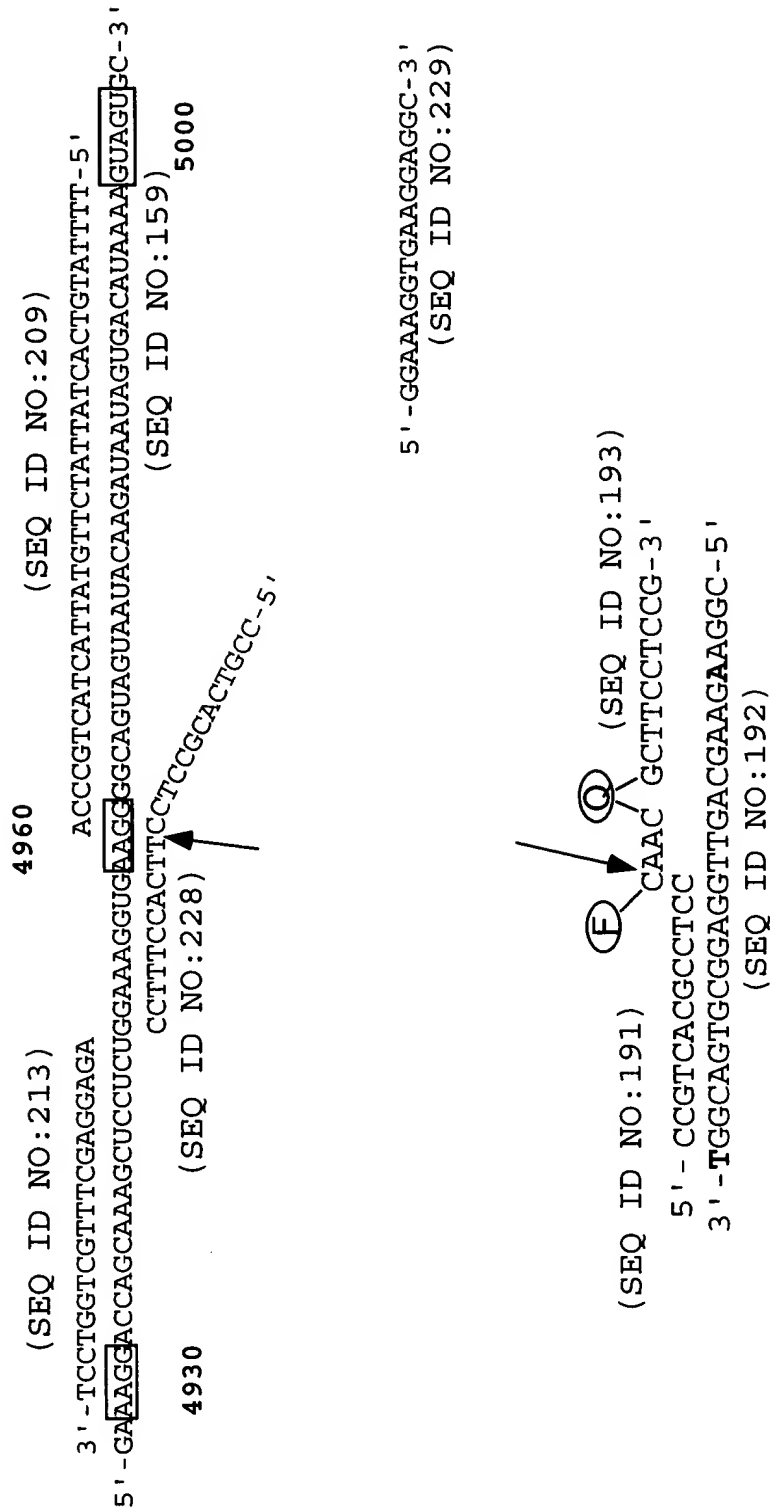


FIGURE 70

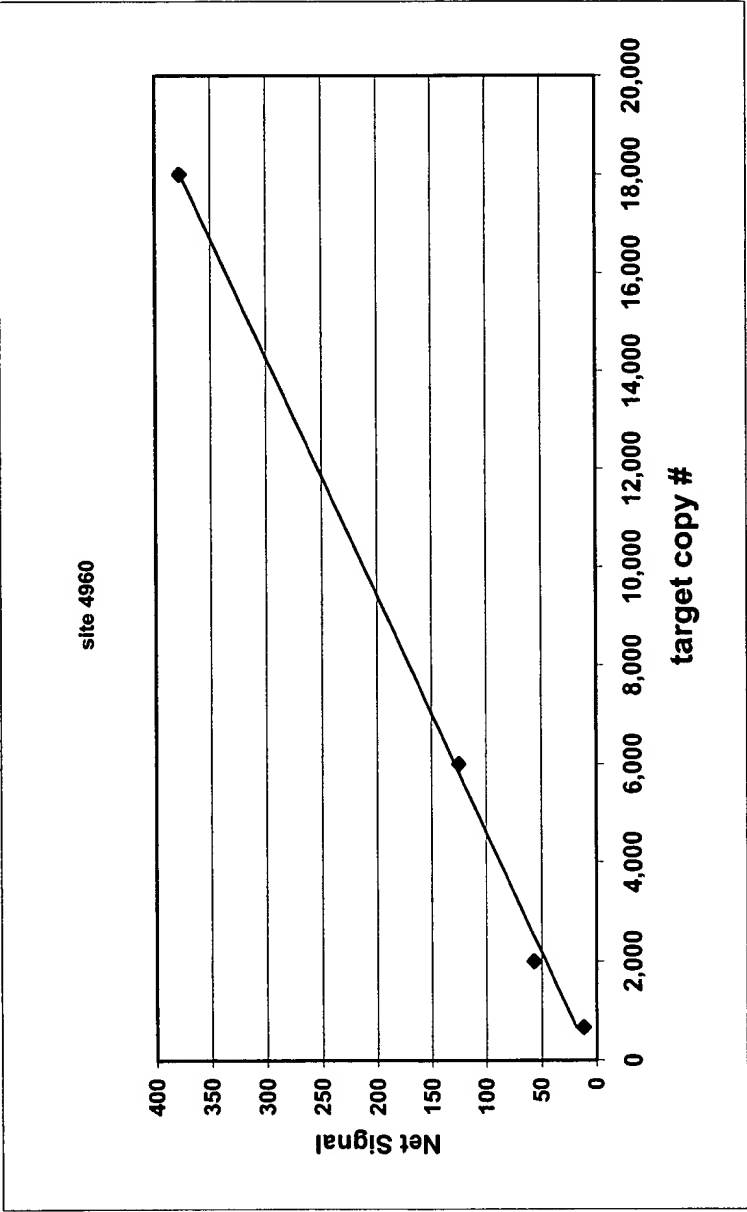


FIGURE 71

Human PSP94

383-31-1 5'-TET-CCTGCTTATCACAATGAA-3' (SEQ ID NO:230)

383-31-3 5'-TET-ACATGCACTTGCTACGAAAC-3' (SEQ ID NO:231)

SEQ ID NO:232

CCUGCUUAUCACAAUGAAUGUUCUCCUGGGCAGCGUUGUGAUCUUUGCCACCUUCGUGA
CUUUAUGCAAUGCAUCAUGCUAUUUCAUACCUAUGAGGGAGUUCAGGAGAUUCAACCA
GGAAUGCAUGGAUCUCAAGGAAACAAACACCCAAUAAACUCGGAGUGGCAGACUGAC
AACUGUGAGACAUGCACUUGCUACGAAACAGAAAUUUCAUGUUGCACCCUUGUUUCUAC
ACCUGUGGGUUAUGACAAAGACAAACUGCCAAAGAAUCUUCAAGAAGGAGGACUGCAAGU
AUAUCGUGGUGGAGAAGAAGGACCCAAAAAAGACCUGUUCUGUCAGUGAAUGGAUAAUC
UAAUGUGCUUCUAGUAGGCACAGGGCUCCAGGCCAGGCCUCAUUCUCCUCUGGCCUCUA
AUAGUCAAAUGAUUGUGUAGCCAUGCCUAUCAGUAAAAAGAUUUUUG

FIGURE 72

Human ubiquitin:

520-77-1 5'-TET-CCGCCACCAAAATGC-3' (SEQ ID NO:233)

520-59-2 5'-TET-GCTGGAAGATGGACG-3' (SEQ ID NO:234)

SEQ ID NO:235

CCGCCACCAAAUGCAGAUUUUCGUGAAAACCCUUA^{CGG}GGAAGACCAUCACCCUCGAG
GUUGAACCCUCGGAUACGAUAGAAAUGUA^{AAGGC}CAAGAUCCAGGAUAAGGAAGGAU
UCCUCCUGACAGCAGAGACUGAUCUUUGCUGGCAAGCAGCUGGAAGAUGGACGUACUUUG
UCUGACUACAAUAUUCAAAAGGAGUCUACUCUUAUCUUGUGUUGAGACUU^{CGUGGUGG}
UGCUAAGAAAAGGAAGAAGAAGUCUUACACCACUCCCAAGAAGAAUAAGCACAAGAGAAA
GAAGGUUAA^{GCU}GGCUGUCCUG~~AAAUUAUUAUAAGGUGGAUGAGAAUGGCAAAAUUAGUC~~
~~GCCUUCGUCGAGAGUGCCCUUCUGAUGAAUGUGGUGCUGGGGUGUUUAUGGCAAGUCACU~~
~~UUGACAGACAUUAUUGUGGCAAAUGUUGUCUGA~~

FIGURE 73

HCV-1a 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:240

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUC
UUGGAU[AAACCC]GCUCAAUGCCUGGAGAUUU[GGG]CGUG[CCC]CCGCAAGACUGCU[AGCC]G
AGUAGUGU[UGG]GUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGU[GCACCAUGAG]

FIGURE 74

HCV-1b 5'-UTR:

898-28-02 5'-TET-GGGACACTCCACCATAGATCACTC-3' (SEQ ID NO:241)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGA-3' (SEQ ID NO:239)

SEQ ID NO:242

GGGACACUCCACCAUAGAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUGCAGCCUCCAGGACCCCCCUCCCGGGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCAGGACGACCGGGUCCUUUC
UUGGAUCAACCCGCUCAAUGCCUGGAGAUUUGGGCGUGCCCCCGGAGACUGCUAGCCG
AGUAGUGUUGGUGUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGUGCACCAUGAG

FIGURE 75

HCV 2a/c 5'-UTR:

898-28-01 5'-TET-GGGACACTCCACCATGAATCACTC-3' (SEQ ID NO:236)

898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)

898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)

898-35-03 5'-TET-GACCGGGTCCTTTCTTGGA-3' (SEQ ID NO:239)

SEQ ID NO:243

GGGACACUCCACCAUGAAUCACUCCCCUGUGAGGAACUACUGUCUUCACGCAGAAAGCGU
CUAGCCAUGGCGUUAGUAUGAGUGUCGUACAGCCUCCAGGCCCCCCUCGGGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUUGCCGGAAGACUGGGUCCUUUC
UUGGAUAAAACCCACUCUAUGCCCGGCCAUUUGGGCGUGCCCCCGCAAGACUGCUAGCCGA
GUAGCGUUGGGUUGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCCCC
GGGAGGUCUCGUAGACCGUGCACCAUGAG

FIGURE 76

HCV 3a 5'-UTR:

898-28-03 5'-TET-GGGACACTCCACCATGGATCACTC-3' (SEQ ID NO:244)
898-35-01 5'-TET-CGGGAGAGCCATAGTGGTCTGCGG-3' (SEQ ID NO:237)
898-35-02 5'-TET-ATTTGGGCGTGCCCCCGC-3' (SEQ ID NO:238)
898-35-03 5'-TET-GACCGGGTCCTTTCTTGA-3' (SEQ ID NO:239)

SEQ ID NO:245

GGGACACUCCACCAUGGAUCACUCCCCUGUGAGGAACUUCUGUCUUCACGCGGAAAGCGC
CUAGCCAUGGCGUUAGUACGAGUGUCGUGCAGCCUCCAGGCCCCCCCUC[CCG]GGAGAG
CCAUAGUGGUCUGCGGAACCGGUGAGUACACCGGAAUCGCUGGGGUGACCGGGUCCUUUC
UUGGAA[CAACCC]GCUCAAUACCCAGAAAUUUGGGCGUG[CCCC]CGCGAGAUAC[UAGCCG]
AGUAGUGU[UGG]GUCGCGAAAGGCCUUGUGGUACUGCCUGAUAGGGUGCUUGCGAGUGCC
CCGGGAGGUCUCGUAGACCGU[GCACCAUGAG]

FIGURE 77A

Human Antigen CD36 mRNA Oligonucleotides

726-38-01	5'-ACAAGGGAAGAGAGATGAGGAACCAG-3'	(SEQ ID NO:246)
666-33-01	5'-TTTGCCTTCTCATCACCAATGG-3'	(SEQ ID NO:247)
937-03-01	5'-TET- aaggggaagagagatgag-3'	(SEQ ID NO:248)
937-03-02	5'-TET-aggagtttgcaagaaac-3'	(SEQ ID NO:249)
937-03-03	5'-TET-ggtgctgtccttg-3'	(SEQ ID NO:250)
937-03-04	5'-TET-cagttttggatccttgatg-3'	(SEQ ID NO:251)
937-03-05	5'-TET-aggacgctgagga-3'	(SEQ ID NO:252)
937-03-06	5'-TET-aacaagtcaaaatcttctatg-3'	(SEQ ID NO:253)
937-03-07	5'-TET-caatactgcagatggag-3'	(SEQ ID NO:254)
937-03-08	5'-TET-aagccaggtattgca-3'	(SEQ ID NO:255)
937-03-09	5'-TET-ctattgtttctgcacaga-3'	(SEQ ID NO:256)
937-03-10	5'-TET-aaatgaagaagaacatagga-3'	(SEQ ID NO:257)
937-03-11	5'-TET-ggtcaagccatcaga-3'	(SEQ ID NO:258)

FIGURE 77B

Human Antigen CD36 mRNA (SEQ ID NO:259)

ACAAGGGAAGAGAGAUGAGGAACCAGAGCUUGUAGAAACCACUUUAAUCAUAUCCAGGA
GUUUGCAAGAAACAGGUGCUUAACACUAAUCCACCUCCUGAACAAAGAAAUAUGGGCUGU
GACCGGAAUGUGGGGCUCAUCGUGGGGUGUCAUUGGUGCUGUCCUGGCUGUGUUUGG
AGGUAUUCUAAUGCCAGUUGGAGACCUGCUUAUCCAGAAGACAAUUAAGCAAGUUG
UCCUCGAAGAAGGUACAAUUGCUUUUAAAAUUGGGUAAAAACAGGCACAGAAGUUUAC
AGACAGUUUUGGAUCUUUGAUGUGCAAAAUCCACAGGAAGUGAUGAUGAACAGCAGCAA
CAUUCAAGUUAAGCAAAGAGGUCCUUAUACGUACAGAGUUCGUUUUCUAGCCAAGGAAA
AUGUAACCCAGGACGCUGAGGACAACACAGUCUCUUUCCUGCAGCCCAAUGGUGCCAUUC
UUUGAACCUUCACUAUCAGUUGGAAACAGAGGCUGACAACUUCACAGUUCUCAUCUGGC
UGUGGCAGCUGCAUCCCUAUUCUAUCAAUAUCAAUUGUUCAAUGAUCCUCAUUCAC
UUUAUUAACAAGUCAAAAUCUUCUAUGUCCAAGUCAGAACUUUGAGAGAACUGUUAUGG
GGCUAUAGGGAUCCAUUUUUGAGUUUGGUUCCGUACCCUGUUACUACUACAGUUGGUCUG
UUUUAUCCUUAACAACAUAUCUGCAGAUGGAGUUUAUAAAGUUUUCAAUGGAAAAGAUAA
CAUAAGUAAAGUUGCCAUAAUCGACACUAUAAAGGUAAAAGGAUCUGUCCUAUUGGG
AAAGUCACUGCGACAUGAUUAAUGGUACAGAUCCAGCCUCAUUUCCACCUUUUGUUGAG
AAAAGCCAGGUUUUGCAGUUCUUUUCUUCUGAUAUUUGCAGGUCAAUCUAUGCUGUAUU
UGAAUCCGACGUUAAUCUGAAAGGAAUCCUGUGUAUAGAUUCGUUCUCCAUCCAAGG
CCUUUGCCUCUCCAGUUGAAAACCAGACAACUAUUGUUUUGCACAGAAAAAUUAUC
UCAAAAAAUUGUACAUCUAUUGGUGUGCUAGACAUCAGCAAUGCAAAGAAGGGAGACC
UGUGUACAUUUCACUCCUCAUUUUCUGUAUGCAAGUCCUGAUGUUUCAGAACCUAUUGA
UGGAUUAACCCAAAUGAAGAAGACAUAGGACAUACUUGGAUUAUCAACCUAUAAUG
GAUUCACUUUACA AUUUGCAAAACGGCUGCAGGUCAACCUAUUGGUCAAGCAUCAGAA
AAAAUUAAGUAUUAAGAAUCUGAAGAGGAACUAUAUUGUGCCUAUUCUUUGGCUUAA
UGAGACUGGGACCAUUGGUGAUGAGAAGGCAA

FIGURE 78

Human Ribosomal Protein L5 mRNA

761-47-01 5'-ATGGGGTTTGTAAAGTTG-3' (SEQ ID NO:260)
 761-47-02 5'-GCTGGGTTTAGCTCTCAGCAGCCCGC-3' (SEQ ID NO:261)
 937-05-01 5'-TET- atgggggtttgttaaagtt-3' (SEQ ID NO:262)
 937-05-02 5'-TET- gaagacgacgagagg-3' (SEQ ID NO:263)
 937-05-03 5'-TET- ggatgatagttcgtgtg-3' (SEQ ID NO:264)
 937-05-04 5'-TET- gctgcagcatattgta-3' (SEQ ID NO:265)
 937-05-05 5'-TET- ctgctatttggatgca-3' (SEQ ID NO:266)
 937-05-06 5'-TET- gcagaagtacatcgga-3' (SEQ ID NO:267)
 937-05-07 5'-TET- gacatgatggaggaga-3' (SEQ ID NO:268)
 937-05-08 5'-TET- agaagaaggatcggg-3' (SEQ ID NO:269)

SEQ ID NO:270

AUGGGGUUUGUUAAGUUGUUAAGAAUAAGGC CUACUUUAAGAGAUACCAAGUGAAAUU
 UAGAAGACGACGAGAGGGUAAAACUGAUUAUUAUGCUCGGAAACGCUUGGUGAUACAAG
 AUAAAAUAAAUACAAACACACCCAAAUAACAGGAUGAUAGUUCGUGUGACAAACAGAGAU
 AUCAUUUGUCAGAUUGCUUAUGCCC GUUAUAGAGGGGGAUAUGAUAGUCUGCGCACGUUA
 UGCACACGAACUGCCAAAUAUGGUGUGAAGGUUGGCCU GACAAAUAUGCUGCAGCAU
 AUUGUACUGGCCUGCUGCUGGCC CGCAGGCUUCUCAAUAGGUUUGGCAUGGACAAGAUC
 UAUGAAGGCCAAGUGGAGGUGACUGGUGAUGAAUACAAUGUGGAAAGCAUUGAUGGUCAG
 CCAGGUGCCUUCACCUGCUAUUUGGAUGCAGGCCUUGCCAGAACUACCACUGGCAAUAA
 AGUUUUUGGUGCCUGAAGGGAGCUGUGGAUGGAGGCUUGUCUAUCCCUACAGUACCA
 AACGAUUCCCU GGUUAUGAUUCUGAAAGCAAGGAUUUAAUGCAGAAGUACAUCGGAAG
 CACAUC AUGGGCCAGAAUGUUGCAGAUUACAUGC GC UACUUAUUGGAAGAAGAUGAAGA
 UGCUUACAAGAAACAGUUCUCUCAUAUACAUAAGAACAGC GUAACUCCAGACAUGAUGG
 AGGAGAUGUAUAAGAAAGCUAUGCUGCUAUA CGA GAGAAUCCAGUCUAUGAAAGAAG
 CCCAA GAAAGAAGUUAAAAA GAAGAGGUGGAACCGUC CCAAAAUGUCCCUU GCU CAGAA
 GAAGGAUCGG GUAGCUCAAAAGAAGGCAAGCUUCCUCAGAGCUCAGGAGCGGGCUGCUG
 AGAGCUAAACCCAGC

FIGURE 79A

**Mouse Scavenger Receptor Class B Type I mRNA
Oligonucleotides**

726-39-01	5'-GCTCAAGAATGTCCGCATAGACCCG-3'	(SEQ ID NO:271)
666-34-01	5'-CTGGTCCCTGAGTTGTTTTTGC-3'	(SEQ ID NO:272)
937-01-01	5'-TET- GCTCAAGAATGTCCG-3'	(SEQ ID NO:273)
937-01-02	5'-TET- gggatgtggaaggag-3'	(SEQ ID NO:274)
937-01-03	5'-TET- ggaccctatgtctacag-3'	(SEQ ID NO:275)
937-01-04	5'-TET- acatcttggtcctgg-3'	(SEQ ID NO:276)
937-01-05	5'-TET- tctcaacacgtacctc-3'	(SEQ ID NO:277)
937-01-06	5'-TET- cggactcagcaaga-3'	(SEQ ID NO:278)
937-01-07	5'-TET- caaggggtgtttgaagg-3'	(SEQ ID NO:279)
937-01-08	5'-TET- ctctgtttctctccca-3'	(SEQ ID NO:280)
937-01-09	5'-TET- gtgaagatgcagctg-3'	(SEQ ID NO:281)
937-01-10	5'-TET- agctggtgctgatg-3'	(SEQ ID NO:282)
937-01-11	5'-TET- caggcctactctgag-3'	(SEQ ID NO:283)
937-01-12	5'-TET- ggactctctcagcg-3'	(SEQ ID NO:284)

FIGURE 79B

Mouse Scavenger Receptor Class B Type I mRNA (SEQ ID NO:285)

GCUCAAGAAUGUCCGCAUAGA[CCC]GAGCAGCCUGUCCUUCGGGAUGUGGAAGGAGAUCC
 CCGUCCCUUUCUACUUGUCUGUCUACUUCUUCGAAGUGGUCAACCCAAAC[GAG]GUCCUC
 AACGGCCAGAAGCCAGUAGU[CCGGG]AGCGUGGACCCUAUGUCUAC[AGG]GAGUUCAGACA
 AAAGGUCAACAUCACCUUCAUGA[CAACGACACC]GUGUCCUUCGUGGAGAA[CCGCAGC]C
 UCCAUUUCAGCCUGACAAGUCGCAUGGCUCAGAGAGUGACUACAUUGUACUGCCUAACA
 UCUUGGUCCUGGGGGGCUCGAUAUUG[AUGGAG]AGCAAGCCUGUGAGCCUGAAGCUGAUG
 AUGACCUUGGCGCUGGUCACCAUGGGCCAGCGUGCUUUUAUG[AACC]GCACAGUUGGUGA
 GAUCCUGUGGGGCUAUGACGAUCCCUUCGUGCAUUUUCUCAACACGUACCUCACAGACAU
 GCUUCCCAUAAAGGGCAAUUGGCCUGUUUGUUGGGAUGAACACUCGAAUUC[UGG]GG
 UCUUCACUGUCUUC[ACGG]GCGUCCAGAAUUC[AGCA]GGAUCCAUCUGGUGGACAAAUGG
 AACGGACUCAGCAAGAUCGAUUAU[UGGCAUUCAGAGCA]GUGUAACAUGAUCAA[UGG]GAC
 U[UCCGG]GCAGAUG[UGGGC]ACCCUUCA[UGACACC]CGA[AUCCUC]GCUGGAAUUCUUCAGCC
 [CGGA]GGCAUGCAGGUCCAUGAAGCUGACCUACAACGAAUCAAGGGUGUUUGAAGGCAUU
 CCCACGUAUCGCUUC[ACGGCC]CCCGAUACUCUGUUUGCCAACGGGUCCGUCUACCCACC
 CAACGAAGGCUUCUGCCCAUGCCGAGAGUCUGGCAUUCAGAAUGUCAGCACCUGCAGGU
 UGGUGCGCCUCUGUUUCUCUCCCACCCCCACUUUAC[AACGCCGAC]CCUGUGUUGUCAG
 AAGCUGUUCUUGGUCUGAACCCUAACCCAAAGGAGCAUUCUUGUUCUAGACAUCCA[U]
 [CCGGU]CACUGGGAUCCCCAUGAACUGUUCUGUGAAGAU[GCA]GC[UGA]GCCUCUACAUCAA
 AUCUGUCAAGGGCAUCGGGCAAACAGGGAAGAUCGAGCCAGUAGUUCUGCCGUUGCUGUG
 GUUCGAACAGAGCGGAGCAAUGGGUGGCAAGCCCCUGAGCACGUUCUACACGCAGCUGGU
 GCUGAUGCCCCAGGUUCUUCACUACGCGCAGUAUGUGCUGCUGGGGCUUGGAGGCCUCCU
 GUUGCUGGUGCCCAUCAUCUGCCAACUGCGC[AGCCAGGA]GAAAUGCUUUUUGUUUUGGA
 GUGGUAGUAAAAAGGGCUCCCAGGAUAAGGAGGCCAUUCAGGCCUACUCUGAGUCCUGA
 UGUCACCAGCUGCCAAGGGCACGGUGCUGCAAGAAGCCAAGCUAUAGGGUCCUGAAGACA
 CUAUAAG[CCCC]CCAAACCUGAUAGCUUGGUCAGACCAGCCACCCAGUCCCUACACCCCG
 CUUCUUGAGGACUCUCUCAGCGGACAGCCCACCAGUGCCAUGGCCUGAGCCCCCAGAUGU
 CACACCUGUCCGCACGCACGGCACAUGGAUGCCCACGCAUGUGCAAAAACAACUCAGGGA
 CCAG

FIGURE 80A

Rat CX3CR1 Accession No. U04808 Oligonucleotides

761-57-01	5'-taatacgactcactatagggacggaagtccaagagcatcactg-3'	(SEQ ID NO:286)
761-57-03	5'-gcaggtacctggtccgta-3'	(SEQ ID NO:287)
781-65-01	5'-TET-ggaagtccaagagca-3'	(SEQ ID NO:288)
781-65-02	5'-TET-aatggcttctttggg-3'	(SEQ ID NO:289)
781-65-03	5'-TET-ggcgtcgccc-3'	(SEQ ID NO:290)
781-65-04	5'-TET-tacttccgcacatcg-3'	(SEQ ID NO:291)
781-65-05	5'-TET-cttcttccctagttgtg-3'	(SEQ ID NO:292)
781-65-06	5'-TET-tgcctggcgt-3'	(SEQ ID NO:293)
781-65-07	5'-TET-gactctactaagaacca-3'	(SEQ ID NO:294)
781-73-01	5'-TET-ccatcttagtggcgt-3'	(SEQ ID NO:295)
781-73-02	5'-TET-caacaagtgcctgg-3'	(SEQ ID NO:296)
781-85-01	5'-TET-aacacggcgtcac-3'	(SEQ ID NO:297)
781-85-02	5'-TET-tgattaccccgagg-3'	(SEQ ID NO:298)
781-85-03	5'-TET-acgctgttttcctg-3'	(SEQ ID NO:299)
781-85-04	5'-TET-tgagacacctgtacaa-3'	(SEQ ID NO:300)
781-85-05	5'-TET-gacggagacagtgg-3'	(SEQ ID NO:301)
781-85-06	5'-TET-caagcgaggagag-3'	(SEQ ID NO:302)

FIGURE 80B

Rat CX3CR1 Accession No. U04808 (SEQ ID NO:303)

GGAAGUCCAAGAGCAUCACUGACAUCUUACCUCCUGAACCUGGCCUUGAGCGACCUGCUC
UUUGUGGCCACUUUGCCCUUCUGGACUCACUACCUCAUCAGCCAUGAGGCCUCCACAA
CGCCAUGUGCAAGCUCACGACUGCUUUCUUCUUAUUGGCUUCUUUGGGGGCAUAUUCU
UCAUCACCGUCAUCAGCAUCGACCGGUACCUCGCCAUCGUCCUGGCCGCCAACUCCAUG
AACAACCGGACAGUGCAACACGGCGUCACCAUCAGUCUGGGCGUCUGGGCGGCGGCCAU
CUUAGUGGCGUCGCCCCAGUUCAUGUUCACAAAGAGAAAGGACAACGAAUGUUUGGGUG
AUUACCCCGAGGUCCUGCAGGAAAUCUGGCCCGUGCUCCGCAACUCGGAGGUCAACAUC
CUGGGCUUCGUCCUGCCCUGCUUAUCAUGAGCUUUUGCUACUUCCGCAUCGUCCGGAC
GCUGUUUUCUGCAAGAACC GGAAGAAGGCCAGAGCCAUAUAGGCUCAUCCUCUUGGUGGU
UGUUGUCUUCUCCUCUUCUGGACGCCUUAACAACUUGUGAUUUUCCUGGAGACUCUCA
AAUUCUACAACUUCUCCCCUAGUUGUGGCAUGAAGAGGGACCUGAGGUGGGCCCUUAGU
GUGACGGAGACAGUGGCGUUUAGCCACUGCUGCCUCAACCCCUUUAUCUACGCUUUCGC
UGGGGAAAAGUUCAGAAGGUACCUGAGACACCUGUACAACAAGUGCCUGGCCGUCCUGU
GCGGUCGUCCUGUCCACGCCGGCUUCUCAACAGAGUCCAGAGGAGCAGGCAGGACAGC
AUUCUGAGCAGCUUGACUCACUACACAAGCGAGGGAGAGGGAUCUCUCCUGCUCUGAAGG
GUCUCCCCGACCCCGACUCUACUAAGAACCCAGAGUCCUGCAUCUGACUCUGUGUAAUG
AAAACAGAUUCACCCCG
CUCCUCCUGCAUUUUAUGUGCAAGAAAUACGGACCAGGUACCUGC

FIGURE 81A

Human Interleukin-1 beta (IL-1 β) Oligonucleotides

720-82-01 5'-
gtaatttaatacgcactcactataggggaaggtgcagttttgccaaggagtgctaaag-3'
(SEQ ID NO:304)

562-15-01 5'-ctgattgaaatcttatctaataaaacatcat-3'
(SEQ ID NO:305)

781-50-01 5'-TET-acttccaagctggc-3' (SEQ ID NO:306)
781-50-02 5'-TET-gagagtggaccacac-3' (SEQ ID NO:307)
781-50-03 5'-TET-gaatcagtgaagatgcc-3' (SEQ ID NO:308)
781-50-04 5'-TET-cattgtaccatgaaatatcc-3' (SEQ ID NO:309)
781-50-05 5'-TET-gaactttaatttcaggaattg-3' (SEQ ID NO:310)
781-50-06 5'-TET-ccctagtctgctagc-3' (SEQ ID NO:311)
781-50-07 5'-TET-ttcaagtgtacttattaacc-3' (SEQ ID NO:312)
781-72-01 5'-TET-aagctggccgtg-3' (SEQ ID NO:313)
781-72-02 5'-TET-tgcagttttgccaag-3' (SEQ ID NO:314)

FIGURE 81B

Human Interleukin-1 beta (IL-1 β) (GenBank Accession #
M15330) (SEQ ID NO:315)

GGCAGAAGUACCUGAGCUCGCCAGUGAAUAUGAUGGCUUAUUAACAGUGGCAAUGAGGAUG
ACUUGUUCUUUGAAGCUGAUGGCACCUAAACAGAUGAAGUGCUCUCCAGGACCUGGAC
CUCUGCCCUCUGGAUGGCGGCAUCCAGCUACGAAUCUCCGACCACACUAACAGCAAGGG
CUUCAGGCAGGCCGCGUCAGUUGUUGUGGCCAUGGACAAGCUGAGGAAGAUGCUGGUUCC
CCUGCCACACAGACCUUCCAGGAGAAUGACCCUGAGCACCUCUUCUCCCUUCAUCUUUGAA
GAAGAACCUAUCUUCUUCGACACAUGGGAUAACGAGGCUUAUGUGCACGAUGCACCUGU
ACGAUCACUGAACUGCACGCUCGCGGACUCACAGCAAAAAGCUUGGUGAUGUCUGGUC
CAUAUGAACUGAAAGCUCCUCCACCUCACAGGACAGGAUAUGGAGCAACAAGUGGUGUUC
UCCAUGUCCUUGUACAAGGAGAAGAAAGUAAUGACAAAUAACCUGUGGCCUUGGGCCUC
AAGGAAAAGAAUCUGUACCCUGUCCUGCGUGUUGAAAGAUGAUAAAGCCACUCUACAGCU
GGAGAGUGUAGAUCCCAAAAUUACCCAAAGAAGAAGAUGGAAAAGCGAUUUGUCUUCAA
CAAGAUAGAAUCAAUAACAAGCUGGAAUUUGAGUCUGCCCAGUUCCCCAACUGGUACAA
UCAGCACCUUCUCAAGCAGAAAACAUGCCCGUCUUCUGGGAGGGACCAAAGGCGGCCAG
GAUAUAACUGACUUCACCAUGCAAUUUGUGUCUUCUAAAGAGAGCUGUACCCAGAGAG
UCCUGUGCUGAAUGUGGACUCAAUCCCUAGGGCUGGCAGAAAGGGAACAGAAAGGUUUU
UGAGUACGGCUAUAGCCUGGACUUUCCUGUUGUCUACACCAAUGCCCAACUGCCUGCCUU
AGGGUAGUGCUAAGAGGAUCUCCUGUCCAUCAGCCAAGGACAGUCAGCUCUCUCCUUUCA
GGCCAAUCCCCAGCCCUUUUGUUUGAGCCAGGCCUCUCUCACUCUCUCCUACUCACUUA
AGCCCGCCUGACAGAAACCACGGCCACAUUUGGUUCUAAGAAACCUCUGUCAUUCGCU
CCCACAUUCUGAUAGCAACCGCUUCCCUAUUUUUUUUUUUUUUUUUUUUUUUUUUUUU
UUCAUUGGUCUAAUUUAUUCAAAGGGGGCAAGAAGUAGCAGUGUCUGUAAAAGAGCCUA
GUUUUUAAUAGCUAUGGAAUCAAUUCAAUUUGGACUGUGUGCUCUCUUUUAAUCAAAGU
CCUUUAAUUAAGACUGAAAAUAUAUAAGCUAGAUUAUUUAAAUGGGAUAUUUAUAA
UGAGCAAAUAUCAUACUGUUA

FIGURE 82A

Human Interferon gamma Oligonucleotides

448-59-01 5'-TET-GCATCGTTTTGGGTTCTCTT (SEQ ID NO:316)
448-59-02 5'-TET-ACTTTAAAGATGACCAGAGC (SEQ ID NO:317)
448-79-01 CACATTGTTCTGATCATCTG (SEQ ID NO:318)
448-79-02 CGGTAAGTGAATGTC (SEQ ID NO:319)
448-79-03 TAGTAAGTGAATGTC (SEQ ID NO:320)
448-79-04 GACATTCAAGTCAGTTACCG (SEQ ID NO:321)
498-20-01 AATTTAATACGACTCACTATACACATTGTTCTGATCATCTG
(SEQ ID NO:322)

498-20-02 AATTTAATACGACTCACTATACGGTAAGTGAATGTC
(SEQ ID NO:323)

498-20-03 5'-TET-CACATTGTTCTGATCATCTG (SEQ ID NO:324)
498-20-04 5'-TET-CGGTAAGTGAATGTC (SEQ ID NO:325)
498-40-01 5'-
AGTAATTTACGACTCACTATAGGGACACATTGTTCTGATCATCTGAAGA
(SEQ ID NO:326)

498-40-02 5'-
AGTAATTTACGACTCACTATAGGGACGGTAAGTGAATGTCCAAC
(SEQ ID NO:327)

498-84-01 5'-TET-CATTCAGATGTAGCG (SEQ ID NO:328)
498-84-02 5'-TET-GACTCATCAATCAAA (SEQ ID NO:329)
498-84-03 5'-TET-GATTACAAGGCTTTA (SEQ ID NO:330)

FIGURE 82B

Human Interferon gamma (SEQ ID NO:141)

CACAUUGUUCUGAUCAUUCUGAAGAUCAGCUAUUAGAAGAGAAAGAUCAGUUAAGUCCUUU
GGACCUGAUCAGCUUGAUACAAGAACUACUGAUUUAACUUCUUUGGCUUAAUUCUCUC
GGAAACGAUGAAAUAUACAAGUUUAUUCUUGGCUUUUCAGCUCUGCAUCGUUUUGGGUUC
UCUUGGCUGUUACUGCCAGGACCCAUAUGUACAAGAAGCAGAAAACCUUAAGAAAUAUU
UUAUGCAGGUCAUUCAGAUGUAGCGGAUAAUGGAACUCUUUUCUUAGGCAUUUUGAAG
AAUUGGAAAGAGGAGAGUGACAGAAAAUAUAGCAGAGCCAAAUUGUCUCCUUUUACUU
CAAACUUUUUAAAAACUUUAAAGAUGACCAGGAUCCAAAAGAGUGUGGAGACCAUCA
AGGAAGACAUGAAUGUCAAGUUUUUCAUAGCAACAAAAAGAAACGAGAUGACUUCGAAA
AGCUGACUAAUUAUUCGGUAACUGACUUGAAUGUCCAACGCAAAGCAAUACAUGAACUCA
UCCAAGUGAUGGCUGAACUGUCGCCAGCAGCUAAAACAGGGAAGCGAAAAAGGAGUCAG
AUGCUGUUUCGAGGUCGAAGAGCAUCCCAGUAAUGGUUGUCCUGCCUACAUAUUGAAU
UUUAAAUCUAAAUCUAUUUAUUAUAUAACAUAUUAUUAUUGGGGAUAUAUUUUUAGAC
UCAUCAAUCAAUAAGUAUUUAUAUAUAGCAACUUUUGUGUAAUGAAAAUGAAUAUCUAUU
AAUAUAUGUAUUUAUUUAUAUUAUCCUAUAUCCUGUGACUGUCACUAAUCCUUUGUUUU
CUGACUAAUAGGCAAGGCUAUGUGAUUACAAGGGCUUUAUCUCAGGGGCCAACUAGGCA
GCCAACCUAAGCAAGAUCCCAUGGGUUGUGUGUUUAUUUCACUUGAUGAUACAUGAAC
ACUUUAAGUGAAGUGAUACUAUCCAGUUACUA

FIGURE 83A

Pneumocystis carinii (NUCLEOTIDES 84-415 OF ACCESSION #
AF236872) (SEQ ID NO:331)

GAGGGUCAUGAAAGCGGCGUGAAAACGUUAGCUAGUGAUCUGGAUAAAUUCAGAUUGC
GACACUGUCAAUUGCGGGGAAGCCCUAAAGAUUCAACUACUAAGCAGUUUGUGGAAAC
ACAGCUGUGGCCGAGUUAUAGCCCGUGGUUAUAGUAAACAAUGUUGAAUAUGAAUCUUUU
GCGAGAUGAAAUGGGUGAUCCGCAGCCAAGUCCUAAGGGCAUUUUUGUCUAUGGAUGCAG
UUCAACGACUAGAUGGCAGUGGUUAUUGUAAGGAAUUGCAGUUUUCUUGCAGUGCUUAA
GGUAUAGUCUAUCCUCUUUCGAAAGAAAGAGUAUUAU

Candida albicans (NUCLEOTIDES 72-418 OF ACCESSION #
X74272) (SEQ ID NO:332)

GGGAGGCAAAAGUAGGGACGCCAUGGUUUCAGAAAUGGGCCGCGGUGUUUUUGACCUGC
UAGUCGAUCUGGCCAGACGUAUCUGUGGGUGGCCAGCGGCGACAUAAACCUGGUACGGGG
AAGGCCUCGAAGCAGUGUUCACCUUGGGAGUGCGCAAGCACAAAGAGGUGAGUGGUGUA
UGGGGUUAAUCCCGUGGCGAGCCGUCAGGGCGCGAGUUCUGGCAGUGGCCGUCGUAGAG
CAGCGAAAGGUAUGGGCUGGCUCUCUGAGUCGGCUUAAAGGUACGUGCCGUCCACACGA
UGAAAAGUGUGCGGUGCAGAAUAGUUCCACAGAACGAAGCUGCGCCGGAGAAAGCGAUU
UCUUGGAGCAAU

FIGURE 83B

Earwig R2 element (SEQ ID NO:333)

UAGGAUGAUAGCGCACCUGGUCAUCGUCUCUCUCAGCUGCUCACUUGCUGUUCUAAGUG
AUAAUACCGUUGUUUUUUAGUGGGUAUUCUUUACGCUUUCGUAGGAGCGAGUCCCAC
ACUCUUGGAGCAAUCCGGGGUAGUGCCUAAACGCAUUUCUUAACGU

Bombyx mori R2 element (SEQ ID NO:334)

GCCUUGCACAGUAGUCCAGCGGUAAGGGUGUAGAUCAGGCCCGUCUGUUUCUCCCCCGGA
GCUCGCUCCCUUGGCUUCCCUUAUAUAUUUUAACAUCAGAAACAGACAUUAAACAUCUA
CUGAUCCAAUUUCGCCGGCGUACGGCCACGAUCGGGAGGGUGGGAAUCUCGGGGGUCUU
CCGAUCCUAAUCCAUGAUGAUUACGACCUGAGUCACUAAAGACGAUGGCAUGAUGAUCC
GGCGAUG

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